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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Identification of novel e2f target genes Patent: WO 2004035798-A 1817 29-APR-2004,
CropDesign N.V. (BE)
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AX101038 Sequence
                                                                                           December 30, 2004, 06:15:28 ; Search time 5051 Seconds (without alignments) 3192.593 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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                                                                   PAT 10-APR-2001
                                                                                                                   Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                   Dean,C. and Levy,Y.Y.
Methods and means for modification of plant flowering characteristics
Patent: WO 0121822-A 10 29-MAR-2001;
Plant Bioscience Limited (GB)
Location/Qualifiers
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TITLE VRNI, a gene required for response to vernalization JORNAL Upublished 3 (bases 1 to 153) AUTHORS Levy, Y. Y. and Dean, C. JULIE Direct Submission JORNAL Submitted (23-JUL-2000) Molecular Genetics, John Innes Centre, Colney Lear, Norwich, Norfolk NR4 7UH, UK PEATURES Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location-Grantsme="Arabidopsis thaliana"	Alignment Scores: 1796.00 17
	0y 281 LeualadiulyaGinTrpProValArgCysLeuTyTLysAlaGlyArgAlaLysPheSer 300

00 00 00 00 00 00 00 0	301 GlnGlyTrpTyrGluPheThrLeuGluAsnAsnLeuGlyGluGlyGspValCysValPhe 320 301 GlnGlyTrpTyrGluPheThrLeuGluAsnAsnLeuGlyGluGlyGspValCysValPhe 320 1169 CaAGGATGGTACGATCACTTAGAGAACTAGAGAAGGAAGAGAGACGTCTTT 122 321 GluLeuLeuArgThrArgAspPheValleuLysValThrAlaPheArgValAsnGluTyr 340 1229 GAGCTGCTCAGAACCAGAGATTCGTTTTTAAAAGTGACCTTTCGAGTCAACGAGTAC 128
111 ProSerProLauProCluserThrValProAlaAshLysGlyYrAlaSerSerNalle 160 22 CALCHOLLINIAN CONTROLOGORANAGOSTANGCANA	=="unassigned DNA" "Taxon:32630" "Taxon:32630" "Tal mutation" "138 Length: "Macches "Conserve" "Mismatc

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Arabidopsis thaliana reduced vernalization response 1 (VRN1) gene, AP289051
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                                                                                                                                    240
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 5000)
Levy, Y. Y., Mesnage, S., Mylne, J.S., Gendall, A.R. and Dean, C.
Multiple roles of Arabidopsis VRNI in vernalization and flowering
time control.

Science 297 (5579), 243-246 (2002)
                                                                                                                                 LeuProSerGlyPheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysValGln
                                                                                                                                                                                                                                                                                                                 281 LeualaGluLyaGlnTrpProValArgCyaLeuTyrLysAlaGlyArgAlaLysPheSer
                                                                                                                                                                                                                                                                                                                                  1108 CTTGCGGAGAAAACAATGGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                      321 GluLeuLeuArgThrArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyr
                  LysLysArgGlyArgLysLysLysAsnAlaAspProGluGluIleAsnSerSerAlaPro
                                201 ArgaspaspapproGluasnArgSerLysPheTyrGluSerAlaSerAlaArgLysArg
                                                                                                     868 CGAGATGATCCAGAGAACCGTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAGAGA
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Direct Submission
Submission
Submitted (23-JUL-2000) Molecular Genetics, John Innes Centre, Colney Lane, Norwich, Norfolk NR4 7UH, UK
Location/Qualifiers
1.5000
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2 v/y.Y., Gendall.A.R. and Dean,C.
VRNI, a gene required for response to vernalization Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                689 CCATCACCACTTCCTGAGTCTACAGTACCAGCCAACAAGGGTATGCTAGTTCAGCCATC 748
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                       Dean, C. and Levy, Y.Y. Methods and means for modification of
                                                                                                                                                                                                                                                Characteristics
Patent: WO 0121822-A 13 29-MAR-2001;
Plant Bioscience Limited (GB)
Location/Qualifiers
                                                                             AX101039 1494 bp
Sequence 13 from Patent WO0121822.
AX101039
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99.71%
99.44%
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synthetic construct
artificial sequences.
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Best Local Similarity:
                        Grc 1291
Val 341
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	Oy 189 ASDAIAASDERO 192	Qy 193Gludluile 195	Qy 196 AsnSerSeralaProArgAspAspAspProGluAsnArgSerIvgPheTyrGluSerAla 215	Oy 216 SeralaargLysArgThrValThrAlaGluGluArgGluArgAlaileAsnAlaalaLys 235 	Qy 236 ThrPheGluProThrAsnProPhePheArgValValLeuArgProSerTyrLeuTyrArg 255	Oy 256 GlyCysileMet	TyrleuProSerGlyPhe 	Qy 266 AlaGluLysFyrLeuSerGlyIleSerGlyPheIleLysValGlnLeuAlaGluLysGln 285	Oy 286 TrpProValArgCysLeuTyrLysAlaGlyArgAlaLysPheSerGlnGlyTrpTyrGlu 305	Db 4200 TGGCCTGTTCGATGTCTCTACAAAGCCGGAGAGCCAAATTCAGTCAAGATGGTACGAA 4259	4260		RESULT 7 APO00735/C LOCUS APO00735 79186 bp DNA linear FLN 14-FEB-2004 DEFINITION Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:Kl3E13.	>	Ē	REFERENCE 1 AUTHORS Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S. TITLE Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC		REFERENCE 2 (bases 1 to 7918) AUTHORS Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S. TITLE Direct Submission	
/ecotype="Landsberg erecta" qene <1879>4370	∕ .u.4	/gene="VRN1" /allele="Ler" join(1879). 1938,31203567,36643732,38324031, 41224370)	/gene="VRN1" /allele="Ler" /note="contains two VP1/ABI3-like B3 domains" /note = contains two VP1/ABI3-like B3 domains"	/product="reduced vernalization response 1" /protein id="AAM76972.1" /db_xref="G1:21734794"." /translation="MPRPPFHX.IPSSTIOEKRLRVPDKFVSKFKDELSVAVALTVPD	GHVMRVGLRKADNKIWFQDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEI NYHSTGLMDSAHNHFKRARLFEDLEDEDAEVIFPSSVYPSPLPESTVPANKGYASSAI. QTLFTGPVKAERPTPKTPKKRRKKKRANDFBENSSAFRDDDPENRSKFYESSAR KRTYTREERRAINAAKTFEPTNPFRYVURFSYLYRGCIMYLPSGFAEKYLSGISGF	TAVQUABEAQUEVA PRVNEYV ORIGIN	Alignment Scores: 1.31e-123 Length: 5000 Score: 1614.50 Matches: 321 Percent Similarity: 77.16% Conservative: 0	: 77.16% Mismacches: 89.89% Indels: 8 Gaps:		Qy 21 ArgvalProAspLysPheValSerLysPheLysAspGluLeuSerValAlaValAlaLeu 40	Oy 41 ThrValProAspGlyHisValTrpArgValGlyLeuArgLysAlaAspAsnLysIleTrp 60	3240	81 3300	Qy 101 GlulleAsnTyrHisSerThrGlyLeuMetAspSerAlaHisAsnHisPhelyBArgAla 120	Oy 121 ArgLeuPheGluAspLeuGluAspGluAspAlaGluValIlePheFroSerSerValTyr 140	141	Oy 161 GlnThrLeuPheThrGlyProValLyB	169	Db 3600 TATCGCTGATTACGCGTCTTATCATTTTGAGGTTGATATTTTCCTTATCT 3659 Qy 170AlaGluGluProThrProThrProLys1leProLysLysLysLysLysLysLysLys

COMMENT

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// note="unnamed protein product; gb|AAC69119.1
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AVCCERWLEPQEHHRYQCRREYKITDKIYILGEDNKVDEVGSGEGEATDSLEGISQVI
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(evidence=not_experimental
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Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=Kl3El3
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.orml.gov/Grail-1.3/)
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGenes (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremulni.zool.iastate.edu/cgi.bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/)
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MCB22 and the 3' clone is MHP21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /trānslation="MKTIQEQLPNDLVEEILCRVPATSLRRLRSTCKAWNRLFKGDRI
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NKVKDWYXIVQEDNVVTEVĢFGVDEMDGCRAVILAYVPSLVQIERAGGNRKRGH"
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ELKRSYSFECERESESERVTMEPATVSPWRYRRSTWNKRQSPFGNLISKSRVFSFRYY
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RLHRYDSEGRCWKYLSSVFERNSVEELALPSEDELEDIDYYPGLPFAALFSAFKARGL
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/note="unnamed protein product; gene_id:K13E13.3
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2742. .3977)
/note="unnamed protein product; gb|AAF01602.1
gene id:K13E13.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="unnamed protein product; gb AAC69119.1
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/mol type="genomic DNA"
/db xref="taxon:3702"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene id:K13E13.1
similar to unknown protein"
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/ecotype="Columbia"
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Qy 169	Oy 260
CDS complement (join (27709. 27957, 28048. 28247, 28347. 28409, 20512. 28652) Anote="unnamed protein product; gb Aad43153.1 game id: (131813.10 similar to unknown protein" /codon start=1 /evidence=note experimental /protein.id="BAB01655.1" /db.xref="Gi: 19280116" /translation="MDSAHHPFKRARLFEDLEDEDRAVIPPSSVYPSPLPESTVPANK fyracf="Gi: 19280116" /translation="MDSAHHPFKRARLFEDLEDEDRAVIPPSSVYPSPLPESTVPANK fyracf="Gi: 19280116" /translation="MDSAHHPFKRARLFEDLEDEDRAVIPPSSVYPSPLPESTVPANK fyracf="Gi: 19280116" /translation="MDSAHHPFKRARLFEDLEDEDRAVIPPSSVYPSPLPESTVPANK GYASALQTLFTGPVKEPTPPKIPFKRGGKKKNADPPEINSSAPRDDDFERRSKYYE SAAKKRYVPAERBENINAAKTPEPTPRFFFFLENNLGEGDVCVPELLATRDFV LKVTAFRVNEY" /codon="MDSAHHPFKRARLFEDLEDESTVENNLGEGDVCVFELLATRDFV LKVTAFRVNEY" /codon=gia: (ii) 13131.11 /codon=gia: (ii) 13131.11 /codon=gia: (ii) 13131.11 /protein_id="MDAB0166:1" /product="oxylase-like protein" /product="oxylase-like protein" /product="oxylase-like protein" /product="oxylase-like protein" /protein_id="MDAB0166:1" /db.xref="di: 1928017" /db.xref="di: 1928	Alignment Scores: Socre: Socre: Socre: 15.4.50 Matches: Socre: Matches: 3.21 Socre: Matches: 3.21 Socre: Matches: 3.21 Matches: 0 0 Matches: 0

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TQTSKVPRFEPTNPFFRYULRPSYLYRGCIMYLASGFARKTVANAEEREA
VNAAKTFEPTNPFFRYULRPSYLYRGCIMYLASGFARKYLSGISGFIKVQLGSKQWPV
RCLYKAGRAKKGSGWYEFTVENNLGEGDVCVFELLRTRDFVLKVTAYRVNEYV"
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Brassica rapa cultivar Kwonsim reduced vernalization response 1
                                                                                                                                                                                                                                                                                                  4200 TGGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTCAGTCAAGGATGGTACGAA 4259
                                                                                                                                                                                                                            4140 GCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAGTCCAGCTTGCGGAGAAACAA 4199
                                                                                                                                                                                          285
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1 (bases 1 to 990)

Kwon,S.-J., Park,B.-S., Kim,S.-Y., Choi,H.-S., Lee,M.-C., Kim,J.-S., Lee, M.-C., Kim,J.-S., Lee, M.-T., Lim,K.-B., Kim,J.-A., Lee,M.-R., Jin,Y.-M., Kim,D. and Kim,H.-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 990)

Kwon,S.-J., Park,B.-S., Kim,S.-Y., Choi,H.-S., Lee,M.-C.,
Kwon,S.-J., Lee,S.-I., Lim,K.-B., Kim,J.-A., Lee,M.-R., Jin,Y.-M.,
Kim,D. and Kim,H.-I.
Direct Submission
Submitted (05-DBG-2003) Genomics Division, National Institute of
Agricultural Biotechnology, Seedun-dong 225, Suwon 441-707,
Republic of Korea
                                                                                                                                                                                     AlaGluLysTyrLeuSerGly1leSerGlyPhe1leLysValGlnLeuAlaGluLysGln
                                                            4020 GGTTGCATCATGGTAATAAAAACATCTTAGGAAGACTTAATCTTATCGGTGTCTTCAC
                                                                                                                                            1080 IGAICTCTAAAAGAAGCCTICTGTTTCTGTTTCTCTCAACAGTATCTTCCTTCTGGGTTT
                                                                                                                                                                                                                                                                        286 TrpProValArgCysLeuTyrLysAlaGlyArgAlaLysPheSerGlnGlyTrpTyrGlu
                                                                                                     260 -----TyrLeuProSerGlyPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                        326 ArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyrVal 341
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/organism="Brassica rapa"
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Unpublished
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AY517929
                   GlyCysileMet
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                       256
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VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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REFERENCE
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3480 CCATCACACTTCCTGAGTCTACAGTACCAGCAACAAAGGGTATGCTAGTTCAGCCATC 3539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3540 CAAACCTIGITCACIGGACCAGITAAAGGIGALAITTALAACCAACIGAITCCCTITAIC 3599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3660 CCAGCTGAAGGCCAACGCCAACCCCAAAAATACCTAAAAAGAGAGGAGGAAGAAGAAGAA 3719
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                                                                                                                                                                                                                                                                                       ArgValProAspLy8PheValSerLy8PheLy8AspGluLeuSerValAlaLeu
                                                                                                                                                                                                                                                                                                                     3120 AGGGTCCCAGATAGTTTGTGAGTAAATTCAAGGATGAGCTTTCGGTTGCTGTTGCACTC
                                                                                                                                                                                                                                                                                                                                                                       ThrValProAspGlyHisValTrpArgValGlyLeuArgLysAlaAspAsnLysIleTrp
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                                                                                                 5000
320
0
1
95
                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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DNA
                                                                                                                                                                                                                                                (1-5000)
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/db_xref="taxon:3702"
                                                                                                                                                                                                                                                US-10-088-187A-11 (1-341) x AX101027
                                                                                                 1.56e-122
1601.50
76.92%
76.92%
89.17%
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Best Local Similarity:
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I (bases 1 to 990)

Kwon, S.-J., Park, B.-S., Kim, S.-Y., Choi, H.-S., Lee, M.-C., Kim, J.-S., Lee, S.-I., Lim, K.-B., Kim, J.-A., Hong, K.-Y., Lee, M.-R., Jin, Y.-M., Kim, D. and Kim, H.-I.

Direct Submission

Submitted (23-JUL-2003) Genomics Division, National Institute of Agricultural Biotechnology, Seodun-dong 225, Suwon 441-707,

Republic of Korea

Location/Qualifiers

I. 990

Adarea "Rema"

Adarea "Rema"
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Brassica rapa cultivar Samjin :
mRNA, complete cds.
AY356368
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                                                                                                                                                                                                                                                                           collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN Arbidopais Full-Length CDNA'): Seki,M', Narusaka,M', Ishida,J', Satou,M', Kamiya,A', Sakurai,T', Carninci,P', Kawai,J', Hayashizaki,Y' and Shinozaki,K'
                                                                                                                                                                                                                                                                                                                                                                                                The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen,M., Soutbwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Johns,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.
                                                                                                                            Center,
, CA 94304,
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Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission
Submitted (25-JUN-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 9430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nguyen, M., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIS. Location/Qualifiers
                                                                                                                                                                                                                                                      RIKEN Genomic Sciences Center (GSC) members carried out
                                                                                                                                                                                                     e-mail for correspondence: arab@sequence.stanford.edu
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F1 CDNA.
                                                                        CTTTGATCTTTAGATACGAAGGCAACTCTGCCTTCAGCGTGTGCATTTACAACTTACA 300
                                                                                                                                            99 HisSerGluIleAsnTyrHisSerThrGlyLeuMetAspSerAla-----HisAsnHis 116
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryopsis viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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  ATTIGGITICAAGAIGGITGGCAAGAGITIGITGACCGITACICCAICCGCAITGGITAC 240
                                                                                                                                                                                                                                                 PhelysArgAlaArgLeuPheGluAspLeuGluAspGluAspAlaGluValIlePhePro 136
                                                                                                                                                                                                                                                                                                                                                    SerSerValTyrProSerProLeuProGluSerThrValProAlaAsnLysGlyTyrAla 156
                                              LeuLeuIlePheArgTyrGluGlyAanSerAlaPheSerValTyrIlePheAsnLeuSer
                                                                                                                                                                             CAGTCCGAGATTAACTACCATTCCACCGGTCTCATGGACTCTGCATCACACAACAACAA
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Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M.,
Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 CAAACCTCAAAAGTTCCTAAAAAGAGGGAGGAAGAAGAAGAAGAATGCTGATCATCCTGAG
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e-mail for correspondence arabosequence.stanford.edu
Genes with similarity to proteins in the databases are described
as 'putative', '-like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://gnomic.cranford.edu/~chris/GENSCAN (Chris Burge,
http://gnomic.cranford.edu/~chris/GENSCAN (Laboratory,
NatplantGene (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/NerplantGene.html) and
ewotif(Nevill-Manning, C.G. Wu, T.D. & Brutlag, D.L.,
http://motif.stanford.edu/projects.html).
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/db_xref="G1:5430747"
/db_xref="G1:5430747"
/db_xref="G1:5430747"
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/db_xref="G1:543077"
/db_xref="G1:54307"
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AFRHFWLAYMKDNSCRFKELSSMACDVLSIPITTVASESSFSIGSGVLSKYRSSLLP
ENIQALICTRNWLRGFPKEGEEEEVEEEKEEEKEERREE
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                                                                                                                                         (bases 1 to 125021)

Pederspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Palm, C.J., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.

Direct Submission

Submitted (08-UDN-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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840. .8514,8612. .8939,9020. .9240,9369. .9546,9658.
/gene="Pl3F21.2"
                          (06-MAY-1999) DNA Sequencing and Technology Center, niversity, 855 California Avenue, Palo Alto, CA 94304,
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
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/gene="F13F21.1"
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/gene="F13F21.2"
Direct Submission
Submitted (06-MAY-1999) Di
Stanford University, 855
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/clone="F13F21"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 155021)
Federspiel, N. P. Palm. C.J., Conway, A.B., Conn, L., Hansen, N.F.,
Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buchler, E., Dunn, P.,
Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S.,
Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vysotskaia, V.S.,
Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pTyrGlupheThrLeuGluhsnAsnLeuGlyGluGlyAspValCy8ValPheGluLeuLe 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
                                                                                                                                                                                                                                                                                                                                                                                                   163 upheThrGlyProValLysAlaGluGluProThrProThrProLysIleProLysLysAr 183
                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCTCTTATGCAAATGGATTCCGCACAGAATCAGTTCAACAAACGTGCTCGATTGTTTGA 229
                                                                                                            uAspleuGluAspGluAspAlaGluValllePheProSerSerValTyrProSerProLe 144
                                                                                                                                                                                                                                                             uProGluSerThrValProAlaAsnLysGlyTyrAlaSerSerAla---IleGlnThrLe 163
                                                                                                                                                                                                                                                                                                      Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altefi, H., Aranjo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskana, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rAlagluGluArgGluArgAla11eAsnAlaAlaLysThrPheGluProThrAsnProPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gGlyArgLysLysAsnAlaAspProGluGluIleAsnSerSerAlaProArgAspAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          paspproGluasnargSerLysPheTyrGluSerAlaaSerAlaargLysArgThrValTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 ePheArgValValLeuArgProSerTyrLeuTyrArgGlyCysIleMetTyrLeuProSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rGlypheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysValGlnLeuAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uLysGlnTrpProValArgCysLeuTyrLysAlaGlyArgAlaLysPheSerGlnGlyTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC007504 125021 bp DNA linear PLN 30-OC
Arabidopsis thaliana chromosome I BAC F13F21 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uArgThrArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyrVal 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGAACTCGGGATTTCGTTCTCGAAGTCACCGCCTTTCGTGTCATGAGTATGTG 854
                                                                                                                                                            230 AGATCCTGAAACTCAAAGATGCTAAGGTCATTTATCCATCG---
              AC007504.3 GI:5430745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 125021)
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Unpublished
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REFERENCE
AUTHORS
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KEYWORDS
SOURCE
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gene

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WHTATATUARAAVVALIMGGGSDBEIRERKSYRAKVCULMFOWNDVLDTGELGK
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/ John
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ALKISPRLKEAEVPWHLIAMMMFFTLIKLPGPYYPYWGRLLVPHFANGVLLRALWSMF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAGKDLITGKLTYPKVMGVDNAREYAKRLNREAQEHLQGFDSDKVVPLLSLADYIVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (join(12218. .12318,12359. .12418,12518. .12695,
12784. .12898,12987. .13143,13236. .13410,13500. .13602,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="97% identical to geranyl geranyl pyrophosphate
synthase [Arabidopsis thaliana] gi|2578822."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Unknown protein; Location of ests 164GlgT7
(gi|2764114), 114GlOT7 (gi|2597578), and 114GllT7
(gi|2597579)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Unknown Protein; Location of ests VBVQD12
(gi|757594 and gi|757593)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="F13F21.3"
complement(10370..11380)
/gene="F13F21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (10370. .11380)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (12218. .14173)
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21730. .21921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F13F21.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="F13F21.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F13F21.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28233 GAGCTITCAGTIGITTITIGCACTIACAAIACCTGGAIGGICAIGITIG-CAIGIAGAACTA 28291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28550 ATCTACTGAACCAGTGAATAAAGGTTATGGCGGTTCTACAGCCATCCAAAGCTTTTTCAA 28609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INKVDPNLKFENDRLKRAYIALQAWKKAIYSDPFKTTANWVGSDVCSYNGVYCAPALD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LeuMetAspSerAlaHisAsnHisPhe---LysArgAlaArgLeuPheGluAspLe 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 uSerThrValProAlaAsnLysGlyTyr---AlaSerSerAlaIleGlnThrLeuPheTh 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgiysAlaAspAsniysIleTrpPheGlnAspGlyTrpGlnGluPheValAspArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28352 TCCATTCGGATTGGT-----TTCAGATACAAA------GTTACAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 rGlyProValLysAlaGluGluProThrProThrProLysIleProLysLysArgGlyAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluLeuSerValAlaValAlaLeuThrValProAspGlyHisValTrpArgValGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerileArgileGlyTyrLeuLeuIlePheArgTyrGluGlyAsnSerAlaPheSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrilePheAsnLeu---Ser-HisSerGluIleAsnTyrHisSerThrGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 uGluAspGluAspAlaGluValilePheProSerSerValTyrProSerProLeuProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(28449. .28680,28766. .28965,29065. .29313)/gene="F13F21.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125021
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89
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Mismatches:
                                                           /note="Hypothetical Protein"
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Matches:
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                                                                                                                      /proteIn_id="AAD43152.1"
/db_xref="G1:5430752"
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/protein_id="AAD43153.1"
/db_xref="G1:5430753"
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/gene="F13F21.8"
   23803. .26346
/gene="F13F21.7"
                                                                                            /codon_start=1
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Conservative: 14 Mismatches: 18 Indels: 5 Gaps: 5 Gaps: 5 HispheLysargalaArgLeuPheGluAspLeuGluAsp ICAGTICAACAACGTGCTCGATIGTTTGAAGATCTGAACTC SPheProSerSerValTyrProSerProLeuProGluSerThr I:: :::	149 ValProalaAsnLysGlyTyrAlaSerSerAlaIleGlnThrLeuPheThrGlyPro	268 268 288 217 317 328 328	APOGGI45 APOGGI45 APOGGI45 APOGGI45 DEFINITION LOTUS CORNICULATUS VAR. japonicus genomic DNA, chromosome 2, clone:LjT03H18, TM0262, complete sequence. ACCESSION APOGGI45. GI:29122784 WERSTON REYWORDS LOTUS corniculatus var. japonicus (Lotus japonicus) LOTUS corniculatus var. japonicus (Lotus japonicus) LOTUS corniculatus var. japonicus (Lotus japonicus) Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; cosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus. REFERENCE LOTUS. REFERENCE LOTUS. TITLE AUTHORS Kaneko, T., Asamizu, E., Kato, T., Sato, S., Nakamura, Y. and Tabata, S. TITLE Features and mapping of sixty-two TAC clones which cover the 6.7 Mb
Qy 185 gLysLysAsnAlaAsp-Pro	237 heGlubrothrasnProPhePheArgValValLeuArgProSerTyrLeuTyrArgGlyC	29198 A 324 I 29258 G SULT 13 505578 AXE CUS FINITION SEC CESSION AXE CESSION AXE XWORDS YWORDS TWORDS THE CONTROL AXE ORGANISM AXE ORG	ા ⊶ા ⊶ા

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16673 GGGGTTAGCAAAACTGTGAAAAGGAAGAGGAAGTCTGAAĆĆAAGTAAGTTCTTTTAGCCA 16732
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Medicago truncatula (barrel medic)
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                 16613 GCTGTTGAATTTAAAAGGTCTACTGAAGAATTGAAATTGCGTTATCCTAACAATGAGGAA
                                                                                                                                                                                                              ---AsnSerSerAlaProArgAspAspAspProGluAsnArgSer
                                                                                                                                                                                                                                                                          LysPheTyrGluSerAlaSerAlaArgLysArgThrValThrAlaGluGluArgGluArg
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                   --LysilePro--
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Sato, S.
Direct Submission

Department of Plant Gene Research; 2-6-7 Kazusa DNA Research Institute,
Department of Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu,
Chiba 292-0818, Japan (B-mail:ssato@kazusa.or.jp,
URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),
Fax:81-418-52-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 ProSerSerValTyrProSerProLeuProGluSerThrValProAlaAsnLysGlyTyr 155
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/db_xref="taxon:34305"
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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AUTHORS
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17272

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Direct Submission
Submitted (13-AUG-2004) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                    Direct Submission
Submitted (03-DEC-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
   rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifo
Medicago.
Shaull, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B.,
Cook, D., Kim, D. and Roe, B.A.
Medicago truncatula BAC Clone mth2-23jl
                                                                                                         2 (bases 1 to 243777)
Shall, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cock, D., Kim, D. and Roe, B.A.
Direct Submission
                                                                                                                                                                                               OK 73019, USA 3 (bases 1 to 243777) Shaull, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D. and Roe, B.A. Direct Submission Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon a size is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                          OK 73019, USA
On Aug 3, 2004 this sequence version replaced gl:50540779.
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-MODEL=frame+ p2n.model - DEV=x1h
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-DE-VGT02_1/USFT0 spool/US10088187/runat_29122004_115842_107/app_query.fasta_1.519
-DB-N Geneseq_238ep04 - QFMT=fastap - SUFFIX=rng - MINNATCH=0.1 - LOOPCIA-0
-LOOPEXT=0 - UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi
-LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15
-MODE=LOCAL - OUTFWT=pto - NORN=ext - HEAPSIXEE=500 - MINLEN=0 - MAXLEN=20000000
-USER=US10088187 @CGN 1 1 470 @runat_29122004 115442_107 - NCFU=6 - ICFU=3
-NO WMAP - LANGEQUERY - NEG SCORES=0 - WAIT - DEPELORE-10 - KGAPPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                    nucleic search, using frame_plus_p2n model
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Jatabase

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Result ŝ

Total number

Searched:

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Altering plant characteristics, useful for producing plants for enzyme or pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                   more proteins.
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Claim 1; SEQ ID NO 1817; 134pp; English.

This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up caracteristics. Specifically, it refers to identifying genes that are up care to man-regulated in transgenic plants oversypesshing the heterodimeric capen plant characteristics accordingly. The present invention describes calter plant characteristics are selected from increased vield or calter plant characteristics are selected from increased vield or blomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, blochemistry, signal or blomass, also be useful as positive or lacered photosynthesis, transduction, storage lipid mobilisation and/or altered photosynthesis, cransduction, storage lipid mobilisation and/or altered photosynthesis, each relative to the corresponding wild type plants. Accordingly, these cach relative to the corresponding wild type plants. Accordingly, these during transformation of cells or tissues. The identified genes play a cole in a variety of biological processes such as DNA replication, cell or than such action factors. This polymucleotide sequence is thale cress oDNA repressed 1.3 fold or more in plants overexpressing the EZFa/DPa

Sequence 1026 BP; 295 A; 235 C; 228 G; 268 T; 0 U; 0 Other;

1026 341 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: (1-1026)US-10-088-187A-11 (1-341) x ADN73922 1.57e-176 1796.00 100.00% 100.00% Best Local Similarity: Query Match: Percent Similarity: Alignment Scores:

Met ProArgProPhePheHisLysLeuIlePheSerSerThrIleGlnGluLysArgLeu 20	Argecacecerrente de la respectación de la respectac	ArgValProAspLysPheValSerLysPheLysBaspGluLeuSerValAlaValAlaLeu 40	AGGGTCCCAGATAAGTTTGTGAGTAAATTCAAGGATGAGCTTTCGGTTGCTTGC	ThrValProAepGlyHisValTrDArgValGlyLeuArgLysAlaAspAsnLysIleTrp 60	ACAGTACCTGATGGTCATGTTTGGCGTGTAGGACTAAGGAAAGCTGACAAAATTTGG 180	PheGlnAspGlyTrpGlnGluPheValAspArgTyrSerIleArgIleGlyTyrLeuLeu 80	TTTCAAGGATGGTTGGCAAGAGTTTGTTGACCGTTACTCCATTCGCATTGGTTATCTTTTG 240	IlepheArgTyrGluGlyAsnSerAlaPheSerValTyrIlePheAsnLeuSerHisSer 100	ATTITIAGATATGAAGAAACTCTGCCTTCAGCGTCTACATTTTCAATTTATCCCACTCT 300	GluileasniyrHisSerThrGlyLeuMetAspSerAlaHisBanHisPheLysArgAla 120	GAGATCAATTACCATTCCACCGGTCTCATGGATTCCGCTCACAACCACTTCAAACGCGCC 360	ArgLeuPheGluAspLeuGluAspGluAspAlaGluValIlePheProSerValTyr 140	CGTTTGTTTGAAGACCTTGAAGATGAAGATGCCGAGGTCATCTTTCCTTCTGTGTAC 420	ProSerProLeuProGluSerThrValProAlaAsnLysGlyTyrAlaSerSerAlaIle 160	CCATCACCACTTCCTGAGTCTACAGTACCAGCCAAGGGTATGCTAGTTCAGCCATC 480	GlnThrLeuPheThrGlyProValLysAlaGluGluProThrProThrProLysIlePro 180
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221 ThrvalthtalacluclushygoluargalalledsmalablatysThrPheGlupToThr 661 AccordarcacachanAnacach	& 43	Argaspaspasprogluasnargseriysphetyrgluseralaseralaarglysarg 22
241 AshbrohebheargvalvalLeuargproserTyrLeunyragGlyCysTleMetTyr 251 AACCCTTTCTCAGGGGGTTCTCCAGGCGATCTATAACAGGGTTCATATATA 251 LeubroserGlyPhealaGludysTyrLeuserGlyIll	දු දු	Thrvalthralaglugluarggluargalaileasnalaalaiysthrpheglubrothr 24
261 LeuproSerGlyPheAlaGluLySTyrLeuSerGlyPheIleLysValGln 781 [දු පු	ABNPROPHEPHEARGVAlValLeuArgProSerTyrLeuTyrArgGlyCysIleMetTyr 26
281 LeuAlaGluLysGlnTrpProValargCysLeuTyrLysAlaGlyArgAlaLysPheSer	දු පු	LeuproSerGlyPheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysValGln 28
301 GlnGlyTrpTyGluPherThrLeuGluAsnAsnieuGlyGluGlyAspValCysValPhe 901 ChAGGATGGTACGAATTCATTGAGAAACTTAGGAGAAGGAGACGTTTGTIT	S S	LeualagiulysgintrpProvalargcysLeuTyrlysAlagiyargalalysPheser 30
321 GlubeuLeuArgThrArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyr 961 GAGCTGCTCAGAACCAGAGATTTCGTTTTGAAAGTGACAGGTAC 341 Val 341 1021 GTC 1023 1021 GTC 1023 10246 standard; cDNA; 1495 BP. 10246 standard; cDNA; 1495 BP. 10246; crop; ss. 10246; 11. vernalisation; flowering; crop; ss. 12. vernalisation; flowering;	% d	GlnGlyTrpTyrGluPheThrLeuGluAsnAsnLeuGlyGluGlyAspValCygValPhe 32
341 Val 341 1021 GTC 1023 52446; 40V-2001 (first entry) 1aliana VRN1 coding sequence. 1; vernalisation; flowering; crop; cidopsis thaliana. Location/Qualifiers 2691294 /*tag= a /product= "VRN1" 00121822-A1. SEP-2000; 2000WO-GB003525. SEP-1999; 99GB-00022071. AN-) PLANT BIOSCIENCE LTD. n C, Levy YY; ; 2001-273467/28. SDB; AAB35491.	දු පු	GluLeuleuArgThrArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyr
2446 standard; cDNA; 1495 BP. 52446; WOV-2001 (first entry) naliana VRN1 coding sequence. Location/Qualifiers Location/Qualifiers 2691294 /*tag= a /product= "VRN1" 00121822-A1. SEP-2000; 2000WO-GB003525. SEP-1999; 99GB-00022071. AN-) PLANT BIOSCIENCE LTD. n C, Levy YY; ; 2001-273467/28. SDB; AAB35491.	& g	val GTC
05-NOV-2001 (first entry) A thaliana VRN1 coding sequence. VRN1; vernalisation; flowering; crop; Arabidopsis thaliana. Key CDS /*tag= a //rag= a //rag= a //product= "VRN1" WO200121822-A1. 29-WAR-2001. 13-SEP-2000; 2000WO-GB003525. 17-SEP-1999; 99GB-00022071. (PLAN-) PLANT BIOSCIENCE LTD. Dean C, Levy YY; WPI; 2001-273467/28. P-PSDB; AAB35491.	AAFG ID XX	52446 standard; cDNA; 1495
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Key CDS WO200121822-A1. 29-MAR-2001. 13-SEP-2000; 20 17-SEP-1999; (PLAN-) PLANT E Dean C, Levy Y WPI; 2001-27346 P-PSDB; AAB3545	Sox	Arabidopsis thaliana.
WO200121822-A1. 29-WAR-2001. 13-SEP-2000; 2000WO-GB003 17-SEP-1999; 99GB-00022 (PLAN-) PLANT BIOSCIENCE Dean C, Levy YY; WPI; 2001-273467/28. P-PSDB; AAB35491.	ELLL:	
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                  1049 CTTCCTTCTGGGTTTGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAAGTCCAG
                                                                                                                                                                                                            GlnGlyTrpTvgluPheThrLeuGluAsnAsnLeuGlyGluGlyAspValCysValPhe
      ACCGTGACTGCAGAAGAAGAGAGAGAGCCATCAATGCAGCCAAAAACGTTCGAACCAACA
                                                                                                                                                                       CTTGCGGAGAAACAATGGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTCAGT
                                                                                                                                                                                                                                  CAAGGATGGTACGAATTCACTCTAGAGAACAACTTAGGAGAAGAGGAGAACGTCTGTGTTTT
                                                                                                                                                                                                                                                                         GluLeuLeuArgThrArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyr
                                                                                                                                                                                                                                                                                         1229 GAGCTGCTCAGAACCAGAGATTTCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGTAC
                                                                                            LeuProSerGlyPheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysValGln
                                                                                                                                                      LeuAlaGluLygGlnTrpProValArgCygLeuTyrLygAlaGlyArgAlaLygPheSer
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16-APR-1999;
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23-APR-1999;
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09-MAR-1999;
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01-APR-1999;
06-APR-1999;
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                                                                                       The present invention provides the protein and coding sequences of Arabidopsis thaliana WRN1. This protein is capable of altering the vernalisation responses of a plant. Also provided are a number of PCR primers used to isolate the sequences. The sequences are useful in the production of corp plants, where they are able to control the timing of Ilowering, the duration of vernalisation required, the optimum temperature, or even eliminate the need for vernalisation completely. The present sequence is the VRN1 coding sequence
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Novel VRN1 polynucleotide sequence encoding a polypeptide which alters vernalization response of plant in which VRN1 nucleic acid is expressed, useful for influencing and assessing vernalization phenotype of plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 AGGTCCCAGATAGTTTGTGAGTAAATTCAAGGATGAGCTTTCGGTTGCTGTTGCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 ilePheArgTyrGluGlyAsnSerAlaPheSerValTyrIlePheAsnLeuSerHisSer
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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03-AUG-1999; 04-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 09-AUG-1999; 10-AUG-1999; 112-AUG-1999; 112-AUG-1999; 123-AUG-1999; 123-AUG-1999; 123-AUG-1999; 124-AUG-1999; 125-AUG-1999; 125-AUG-1999; 126-SEP-1999; 127-AUG-1999; 127-AUG-1999; 128-EEP-1999; 128-EEP-1999; 128-EEP-1999; 129-EEP-1999; 130-CCT-1999; 140-CCT-1999; 140-CCT-1999; 140-CCT-1999; 140-CCT-1999; 140-CCT-1999; 140-CCT-1999; 140-CCT-1999; 140-CCT-1999; 150-CCT-1999; 160-CCT-1999; 170-CCT-1999;
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                300 rGlnGlyTrpTyrGluPheThrLeuGluAsnAsnLeuGlyGluGlyAspValCysValPh
          1184 TCAAGGATGGTACGAATTCACTCTAGAGAACAACTTAGGAGAAGGAGGACGTCTGTGTTT
                                                                                                                                                           Arabidopsis thaliana DNA fragment SEQ ID NO: 69061.
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The present invention provides the protein and coding sequences of Arabidopsis thaliana VRNI. This protein is capable of altering the vernalisation responses of a plant. Also provided are a number of PCR primers used to isolate the sequences. The sequences are useful in the production of crop plants, where they are able to control the timing of Ilowaring, the duration of vernalisation required, the optimum temperature, or even eliminate the need for vernalisation completely. The present sequence is the VRNI gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel VRNI polynucleotide sequence encoding a polypeptide which alters vernalization response of plant in which VRNI nucleic acid is expressed, useful for influencing and assessing vernalization phenotype of plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3120 AGGGTCCCCAGATAAGTTTGTGAGTAAATTCAAGGATGAGCTTTCGGTTGCTGTTGCACTC
              TrpProValArgCysLeuTyrLysAlaGlyArgAlaLysPheSerGlnGlyTrpTyrGlu
                          1021 TGGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTCAGTCAAGGATGGTACGAA
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                                                         PheThrLeuGluAsnAsnLeuGlyGlyGlyAspValCysValPheGluLeuLeuArgThr
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                                                                                                       ArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyrVal 341
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                                                             IlepheArgTyrGluGlyAenSerAlaPheSerValTyrIlePheAsnLeuSerHisSer 100
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US-10-088-187A-11 (1-341) x AAC54934 (1-1394)

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                                                                                               uSerAlaSerAlaArgLysArgThrValThrAlaGluGluArgGluArgAlaIleAsnAl
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RESULT

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                Arabidopsis thaliana DNA fragment SEQ ID NO: 75262
standard; DNA; 1396 BP
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17-OCT-2000 (first entry)

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MetProArgProPhePheHisLysLeullePheSerSerThr11eGlnGluLysArgLeu 20

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid array or goods of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abloric stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZINJS-6-ABZINJS-4) used in methods of the invention. Note: The sequence data for this patent is not respresented in the printed specification but is based on sequence information supplied to berwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
                                                                                  GlnGlyTrpTyrGluPheThrLeuGluAsnAsnLeuGlyGluGlyAspValCysValPhe 320
                                                                                                GluLeuLeuArgThrArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyr 340
                                                                                                                                                         543
                                    LeuhlaglulysglnTrpProValArgCysLeuTyrLysAlaGlyArgAlaLysPheSer 300
                                                            423
 GAGCTGCTCAGAACCAGAGATTTCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 144; SEQ ID NO 273; 577pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                    dB.
                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana stress regulated gene SEQ ID NO 273
                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana; plant; gene; stress; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SCRI ) SCRIPPS RES INST.
(SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-AUG-2001; 2001WO-US026685.
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
                                                                                                                                                                                                                                                         ABZ12468 standard; DNA; 681
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                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana.
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681 190

Length: Matches:

1.69e-88 946.00

Alignment Scores: Pred. No.: Score:

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327
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                                                                                                                                                                                                                                                                                                                                                                                              396
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                                                                                110 MetAspSerAlaHisAsnHisPhe---LysArgAlaArgLeuPheGluAspLeuGluAsp 128
                                                                                                                                                                           149 ValproalaasnLysGlyTyr---AlaSerSerAlalleGlnThrLeuPheThrGlyPro 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuGluAsnAsnLeuGlyGluGlyAspValCysValPheGluLeuLeuArgThrArgAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCGAGAACAATATAGGCGAAGGAGATGTATCTGTGTTTGAGCTACTCAGAACTGGGAT
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                                                                                              7 ATGGATTCCGCACAGAATCAGTTCAACAACGTGCTCGATTGTTTGAAGATCCTGAACTC
                                                                                                                                                                                        168 VallysalaglugluproThrProThrProLysileProLysiysakgGlyArgLysiys
                                                                                                                                                                                                                                        ArgSerLysPheTyrGluSerAlaSerAlaArgLysArgThrValThrAlaGluGluArg
                                                                                                                                                                                                                                                                                                                                                                         GluArgAlaIleAsnAlaAlaLysThrPheGluProThrAsnProPhePheArgValVal
                                                                                                                             129 GluaspalaGluvalilePheproSerSerValTyrProSerProLeuProGluSerThr
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14
113
5
           Mismatches:
Indels:
Gaps:
                                                          US-10-088-187A-11 (1-341) x ABZ12468 (1-681)
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87.18%
81.20%
52.67%
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Conservative: Mismatches:

512.00 97.96% 97.96% 28.51%

Indels:

Gaps: (1-426)

Matches:

283 306

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245 TACGAATTCACTCTAGAGAACAACTTAGGAGAAGGAGACGTCTGTGTGTTTGAGCTGCTC 186
                                                                                                                                                                                                                                                                    GlyPheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysValGlnLeuAlaGlu
                                                                                                                                                                         244 PheArgValValLeuArgProSerTyrLeuTyrArgGlyCysIleMetTyrLeuProSer
                                                                                                                                                                                                                          365 GGGTTTGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAAGTCCAGNATGNGGAG
                                                                                                                                                                                                                                                                                                                                                           LysGlnTrpProValArgCysLeuTyrLysAlaGlyArgAlaLysPheSerGlnGlyTrp
                                                                                                                                                                                                                                                                                                                                                                                                        305 AAACAATGGCCTGTTCGATGTCTTCTACAAAGCCGGGAGAGGCCAAATTCAGTCAAGGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TyrGluPheThrLeuGluAsnAsnLeuGlyGluGlyAspValCysValPheGluLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 ArgThrArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyrVal 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 AGAACCAGAGATTTCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGTACGTC 132
                                                                                                                                 US-10-088-187A-11 (1-341) x ABX62122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC03457 standard; DNA; 1361 BP.
              Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an Arabacopsis unaidant anciera actu, it.e.

The invention describes an Arabacopsis unaidate agent (III) or polypeptide (II) encoded by (I), transgenic plant (III) or genetically modified cell (IV) are useful for screening a candidate agent for its biological effect, by combining the candidate agent with (II), (III) or (IV), and determining the effect of the candidate agent on (II), (III) or (IV), is useful for identifying homologous or related genes, for producing compositions that modulate the expression or function of its encoded protein, for mapping functional regions of the protein, in diagnosis, for studying associated physiological pathways, for genetic manipulation of cells, preferably plant cells, in screening assays of various plant strains to determine the strains that are capable of continuing polypeptides, as probes for the detection of mRNA in biological or inhibiting production of biosynthetic product in a plant, for producing polypeptides, as probes for the detection of mRNA in biological camples, to generate additional copies of (I), to generate ribozymes or oligonucleotides, as single stranded DNA probes or as triple-strand for amplement of introducing or improving disease resistance and stress consistence in plants, such as plant cells and plants, (II) or (III) is useful for introducing or improving disease resistance and stress consistence in plants, screening biological active agents, e.g., fungicides, insecticides, etc., and for elucidating biochemical pathways. CC (III) is useful as crops for their enhanced diseased resistance, enhanced tolerance to environmental stress, or to produce a factor. This enquence represents a nucleic acid that may correspond to naturally cocurring Arabidopsis thaliana expressed sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obstance the sequence the may correspond to naturally coversing Arabidopsis thaliana expresses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel Arabidopsis thaliana nucleic acid useful for identifying homologous or related genes, and to create genetically modified and transgenic organisms, such as plant cells and plants.
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: JP, Haas WD;
Hoffman N;
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Ledford BL, Woessner
Davis KR, Allen K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hamilton CM, Pr
A, Mathew AV, L
er M, Slater T,
                                                                                    27-JAN-2000; 2000US-0178512P
                                          26-JAN-2001; 2001US-00770423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rameaka JG, Page A, N
Garcia CA, Kricker M,
                                                                                                                                                        AN Y.
HAMILTON C M.
PRICE J L.
RAINES T M.
                                                                                                                                                                                                                                                                                       PAGE A.
MATHEW A V.
LEDFORD B L.
WOESSNER J P.
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KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
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RAMEAKA J G.
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                                                                                                                                 GORLACH J.
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04-APR-2002
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Rameaka JG,
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The invention comprises the amino acid and coding sequences of proteins involved in the control of flowering time in rice. The DNA and protein sequences of the invention are useful for modulating flower architecture and flowering time, the DNA and protein sequences are useful in the area of plant biotechnology, commercial plant farming and agriculture. The present wheat DNA sequence shows homology to the rice sequences of the
                                                                                                                                                               flowering time; wheat, flower architecture; plant biotechnology; commercial plant farming; agriculture; flowering-related protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid molecule encoding a polypeptide modulating flower architecture and flowering time, useful in the area of plant biotechnology, and commercial plant farming and agriculture.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sessions A, Briggs S, Cooper B, Goff SA, Moughamer T;
Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D,
                                                                               Wheat flowering time-related DNA sequence #17.
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18-DEC-2003 (first entry)
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426

Length:

1.03e-43

Alignment Scores: Pred. No.:

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                                                                                                                                                                                                                                                       313 AATGACCTCTTGCTTTGCATGCACTGGCAATGCCTCCTTCGAGGTCCTAATCTTCGAG 372
                                                                                                                                                                                                                                                                                                                                     97 LeuSerHisSerGlu---IleAsnTyrHisSerThrGlyLeuMetAspSerAlaHisAsn 115
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                                                                                                                                                                                                                                                                                                                                                     116 HisPheLysArgAlaArgLeuPheGluAspLeuGluAspGluAspAlaGluValIlePhe
                                                                                                                                                                                                                                                                                                                                                                                                           433 AATATGGTGGGTCAAGGCGGCGTTGAGCAATACCCTGATTCTGAT---GATACTAGGGTG
                                                                                                                                                                                                               .93 GACCTGAAACTGAAAGCACCGAGAGCGTGAGACATGAGCATGTGGGTGTCAGCAAGGTTGCC
0 U; 0 Other;
                                   1361
93
47
142
31
                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Ë
C; 371 G; 320
                                                                                                                      (1-1361)
                                                                                                Gaps:
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 353 A; 317
                                   8.14e-21
298.50
44.73%
29.71%
16.62%
   BP;
                                                                          Best Local Similarity:
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                                                            Percent Similarity:
   Sequence 1361
                           Alignment Scores:
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60 IrpPheGlnAspGlyTrpGlnGluPheValAspArgTyrSerIleArgIleGlyTyrLeu 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 LeuArgValproAspLysPheValSerLysPheLysAspGluLeuSerValAlaValAla 39
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                                                                                                                                                                                            gene;
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58 ATTAGCATACCGGAGAAAGTTGCGGACAGATTCAGTGGTGGTCAGATCACCAAAGGGTTCAAC
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                                                                                                                                                                             flowering time; rice; flower architecture; plant biotechnology; commercial plant farming; agriculture; flowering-related protein;
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flower architecture and flowering time, useful in the area of J
biotechnology, and commercial plant farming and agriculture.
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F, Kreps J, Provart N, Ricke
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88
56
148
25
Length:
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                                                                                                                                                        #28.
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                                                                                                                                                        Rice flowering time-related gene
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                                                                             ВР
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26-SEP-2001; 2001US-0325277P.
30-NOV-2001; 2001US-0334984P.
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293.50
45.43%
27.76%
16.34%
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                                                                              DNA; 1041
                                                                                                                                entry)
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Glazebrook J, Katagiri
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                                                                                                                                (first
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Best Local Similarity:
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    174 ThrProThrProLysIleProLysLysArgGlyArgLysLysLysAsnAlaAspProGlu 193
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                                                                                                                                               96 AsnLeuSerHisSerGlu---IleAsnTyrHisSerThrGlyLeuMetAspSerAlaHis 114
                                                                                                                                                                                                                                                                ::: ||| |:: ||| 358 GGTCAGAATACCATTTAAGTGATTCTGAAGATACTAGCACA--- 414
                                                                                                                                                                                                                                                                                                                        135 PheproSerSer---ValTyrProSerProLeuProGluSerThrValProAlaAsnLys 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       568 ATGATTGAGGAAGAGAAGAGTGATGATGATGATGAGCATGCTGATTATGAACATGCTGAC 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            628 TACTÁCTACTCGAGGTTTGCC----AATTACCTAÁCTGGCGÁGGÁACGTGÁAGAG--- 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 IleAsnAlaAlaLysThrPheGluProThrAsnProPhePheArgValValLeuArgPro 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 SerGlyIleSerGlyPheIleLysValGlnLeuAlaGluLys-----GlnTrpProVal 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 ArgCysLeuTyrLysAlaGlyArgAlaLysPheSer---GlnGlyTrpTyrGluPheThr 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     859 AAATACTACCATGCAAGCACTACCAGGGCTTCAATTGCCAACGCTGGATCAAGTTCATC 918
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                                                                LeullePhe-----ArgTyrGluGlyAsnSerAlaPheSerValTyrIlePhe
                                                                                                                                                                          308 LeuGluAsnAsnLeuGlyGluGlyAspValCysValPheGluLeuLeuArg 324
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30-AUG-1999;
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04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
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106 SerThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAlaArgLeuPheGluAsp 125

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293 AGTGAGTTTGCAGAGGCTCATTCCATCGAGAGGCCACTTTCTCTTGTTCGAATACAAG 352

66.GlnGluPheValAspArgTyrSerlleArgIleGlyTyrLeuLeulePheArgTyrGlu 85

US-10-088-187A-11 (1-341) x AAC35159 (1-796)

ò 셤 PhevalSerLysPheLysAspGluLeuSerValAlavalAlaLeuThrValProAspGly

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23-SEP-1999; 24-SEP-1999; 26-SEP-1999; 26-SEP-1999; 66-OCT-1999; 66-OCT-1999; 66-OCT-1999; 13-OCT-1999; 13-OCT-1999; 14-OCT-1999; 16-OCT-1999; 16-OC	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:
## ## ## ## ## ## ## ## ## ## ## ## ##	Align Pred. Score Perce Best Query DB:

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126 LeuGluAspGluAspAlaGluValllePheProSerSerValTyrProSerProLeuPro 145	428 ATCATCGACAGGACGATGATAATC454	146 GluSerThrValProAlaAsnLysGlyTyrAlaSerSerAlaIleGlnThrLeuPheThr 165	454 454	166 GlyProValLyBAlaGluGluProThrProThrProLyBIleProLyBLyBArgGlyArg 185		186 LysLysLys-AsnAlaAspProGluGluIleAsnSerSerAlaProArgAspAspAs 204	497 AAAAATAATCTAATCGTTAATGGTGATACAGAGCACAAAATCCAAGAAGAGAGACCAAGA 556	heTyr	:: 557 GACATCGAGTTTGACAAGATTCTACACGATGTTGATGTGGATGCAAGTGCTTAAAGAAGAA 616	3luGluArgGluArgAlaIleAsnAlaAla	
LeuGluAspGluAsp	ATCATCGACAGCGAC	GluSerThrValPro		GlyProValLysAla		Lystystys-AsnAl	AAAAATAATCAATCI	pProGluAsnArgSe	GACATCGAGTTTGACAAGAT	gLysArgThrValTh	Gaagaagacaagaga
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Search completed: December 30, 2004, 06:32:39 Job time : 581 secs

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RESULT 1
US-09-351-457-3
; Sequence 3, Application US/09351457
; Sequence 3, Application US/09351457
; Patent No. 6312694
; GENERAL INFORMATION:
; APPLICANT: THORER, PHILIP E.
; TITLE OF INVENTION: THAT BIND TO AMINOPHOSPHOLIPIDS
; TITLE OF INVENTION: THAT BIND TO AMINOPHOSPHOLIPIDS
; FILE REFERENCE: 4001-002300
; CURRENT APPLICATION NUMBER: US/09/351,457
; CURRENT PILING DATE: 1999-07-12
; SOFTWARE: PATENTING PATE: 2.0
; SOFTWARE: PATENTING PATE: 2.0
; SEQ ID NO 3
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Sequence 1, Appli
Sequence 714, Ap
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Sequence 3647, Ap
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                    nucleic search, using frame_plus_p2n model
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US-09-561-500-3
US-09-561-608-3
US-09-351-543-3
US-09-561-526-3
US-09-998-831-3
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US-08-665-926-5
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Maximum Match 100%
Listing first 45 summaries
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Match
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Scoring table:

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APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
APPLICANT: Roll A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002584
CURRENT APPLICATION WINBER: 04/09/561,108
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR APPLICATION NUMBER: 60/131,432
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN VOY: 2.0
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Patent No. 6342221
GENERAL INFORMATION:
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     1364 TGGAAAGAATATAAAGTGGGATTTGGTAACCCTTCAGGAGAATATTGGCTGGGAAATGAG 1423
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APPLICANT: Rolf A. Brekhen
APPLICANT: Rolf A. Brekhen
TITLE OF INVENTION: ANTHONY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002500
CURRENT PEPLICATION NUMBER: US/09/561,500
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                               GluglyAsnSerAlaPheSerValTyr---IlePheAsnLeuSerHisSerGluIleAsn 103
                                                                                                                                                                                        104 Tyr-----HisSerThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAlaArg
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US-09-351-543-3
; Sequence 3, Application US/09351543
; Patent No. 6406693
; GENERAL INFORMATION:
; APPLICANT: THORPE, PHILIP E.
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TITLE OF INVENTION: CANCER TREATMENT METHODS USING ANTIBODIES TITLE OF INVENTION: AMINOPHOSPHOLIPIDS
FILE REFERENCE: 4001.002200
CURRENT APPLICATION NUMBER: US/09/351,543
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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                                                               ---AlaAlaLysThrPh 237
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APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF
FILE REPREBUCE: 4001.002582
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US/09/561,499
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR PILING DATE: 1999-04-28
SUUMBER OF SEQ ID NOS: 44
SOFTWARE: PALENTIN Ver. 2.0
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                                                                 222 iThralaGluGluArgGluArgAlaIleAsn----
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Batent No. 6416758

GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF
FILE REPERENCE: 4001.002586
CURRENT APPLICATION NUMBER: US/09/561,526
CURRENT PILING DATE: 2000-04-28
REACH APPLICATION NUMBER: 60/131,432
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN VET: 2.0
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Best Local Similarity:
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Sequence 3, Application US/09561005
Patent No. 6703020
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE METHODS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002585
CURRENT APPLICATION NUMBER: US/09/561,005
CURRENT PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR PILING DATE: 1999-04-28
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| Sequence 3, Application US/0999831
| Patent No. 667641
| GENERAL INFORMATION:
| APPLICANT: Philip E. Thorpe
| APPLICANT: Philip E. Thorpe
| TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY
| TITLE OF INVENTION: INHIBITING VEGF
| FILE REFERENCE: 4001.002584
| CURRENT APPLICATION NUMBER: US/09/998,831
| CURRENT FILIG DATE: 2001-11-30
| PRIOR FILIG DATE: 2000-04-28
| NUMBER OF SEQ ID NOS: 44
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US-10-088-187A-11 (1-341) x US-09-819-386-3 (1-2269)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1985 AGAGCCTGTAAAC 1997
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|1724 TACTATCCACAGAGGCAGAACACAAATAAGTTCAACGGCATTAAATGGTACTACTGGAAA 1783
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TTIGTTTCGCAACTGACTATGTGCTTAAAATACACCTTAAAGACTGG 1483
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                                                                                                                                                                                                                                                                                                                 pAspAspProGluAsnArgSerLysPheTyrGluSerAlaSerAlaArgLysArgThrVa 222
                                                                                                                                                                                                                                                                                                                                                        222 lThralaGluGluArgGluArgAlaIleAsn------AlaAlaLysThrPh 237
                                                                                                                                                       138 SerValTyr-----ProGluSe 147
                                                                                                                                                                                              147 rThrValProAlaAsnLysGlyTyrAlaSerSerAlaIleGlnThrLeuPheThrGlyPr 167
                                  GluglyAsnSerAlaPheSerValTyr---IlePheAsnLeuSerHisSerGluIleAsn 103
                                                                        104 Tyr-----HisSerThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAlaArg 121
                                                                                                               122 LeuPheGluhspLeuGluhspGluhspAlaGlu------ValIlePheProSer 137
                                                                                                                                                                                                                                                       (784 GGCTCAGGCTATTCGCTCAAGGCCACAACATGATGATCCGACCAGCAGATT-----
                                                                                                                                                                                                                                                                           sArgGlyArgLysLysLysAsnAlaAspProGluGluIleAsnSerSerAlaProArgAs
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Matches:
Conservative:
Mismatches:
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104.00
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Best Local Similarity:
Query Match:
DB:
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US-09-819-386-3
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1664 CAAATGCTAACAGGGCTGGTGTTGATGCATGTGGTCCTTCCAACTTGAACGGAATG 1723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 rThrValProAlaAsnLysGlyTyrAlaSerSerAlaIleGlnThrLeuPheThrGlyPr 167
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45 GIYHisValTrpArgValGlyLeuArgLysAlaAspAsnLysIleTrpPheGlnAspGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Sequence | Application US/08373579 | Sequence | Application US/08373579 | Sequence | Application US/08373579 | Patent No. 5650490 | GENERAL INFORMATION: | APPLICANT: Davis, et al. | TITLE OF INVENTION: THEREOF | TITLE OF INVENTION: THEREOF | TITLE OF INVENTION: THEREOF | TITLE OF INVENTION: THEREOF | TITLE OF INVENTION: THEREOF | TITLE OF INVENTION: THEREOF | ADDRESSEE: | ADDRESSEE: Regeneron Pharmaceuticals, Inc. | ADDRESSEE: TITLE OF USA. | STATEY | TO did Saw Mill River Road | CITY: TATTYCOWN | STATEY: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New York | STATE: New
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|1731 TACTATCCACAGAGGCAGAACACAAATAAGTTCAACGGCATTAAATGGTACTACTGGAAA 1790
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|1932 |ctctttccaccacaGaGGGCGTGTGCTGGTGCTGACGGGACCCACATGCTCCAGATT 1991
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                                                              147 rThrValProAlaAsnLysGlyTyrAlaSerSerAlaileGlnThrLeuPheThrGlyPr 167
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APPLICANT: Davis, et al.
TITLE OF INVENTION: THE-2 LIGAND, METHOD OF MAKING AND USES TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: Requeron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STRIE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,595
FILING DATE: 06-APR.1995
CLASSIFICATION NUMBER: US 08/373,579
FILING DATE: 17-JAN.1995
APPLICATION NUMBER: US 08/373,579
FILING DATE: US 08/373,579
FILING DATE: US 08/353,503
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-CCT-1994
PRICK APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-CCT-1994
PRICK APPLICATION NUMBER: US 08/330,261
FILING DATE: 07-CCT-1994
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-CCT-1994
ATORNEY AGENT INFORMATION:
NUMBER: CODECT-1994
NUMBER: CODECT-1994
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NUMBER: CODECT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 5, Application US/08418595 ; Patent No. 5814464
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TELEPHONE: (914) 345-7400
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REGISTRATION NUMBER: 36,108
RELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY AGENT INFORMATION:
                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,579
FILING DATE: 17-JAN-1995
                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
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MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
Query Match:
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NAME/KEY:
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US-08-373-579-5
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Pred. No.:
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1932 GICCICITCCACCACAGAGGCGIGGIGCICGAGGACCCACAIGCICCAGAIT 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 rThrValProAlaAsnLysGlyTyrAlaSerSerAlaIleGlnThrLeuPheThrGlyPr 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tyr-----HisSerThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAlaArg 121
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                                                                                                                                                                                                                                                                                                                                                                       PhevalAspArgTyrSerIleArgIleGlyTyrLeuLeu------IlePheArgTyr 84
                                                                                                                                                                                                                                                                      45 GlyHisValTrpArgValGlyLeuArgLysAlaAspAsnLysIleTrpPheGlnAspGly 64
                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 SerValTyr-------
SEQUENCE CHARACTERISTICS:
LENGTH: 2282 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
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|992 AGAGCCTGTAAAC 2004
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104.00
37.55%
23.67%
5.79%
                                                                                                         357..1847
                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                             , NAME/KEY:
; LOCATION:
US-08-418-595-5
                                                                                                                                               Alignment Scores
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|1371 TGGAAAGAATATAAAGTGGGATTTGGTAACCCTTCAGGAGAATATTGGCTGGGAAATGAG 1430
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TTTGTTTCGCAACTGACTAATCAGCAACGCTATGTGCTTAAAATACACCTTAAAGACTGG 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluGlyAsnSerAlaPheSerValTyr---IlePheAsnLeuSerHisSerGluIleAsn 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tyr-----HisSerThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAlaArg 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TrpGln------Glu
                                                     GENERAL INFORMATION:
APPLICANT: Valenzuela et al.
TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Requeron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2282
58
34
92
61
                                                                                                                                                                                                                                                                                                        COMPUTER KEALMILE FORM
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,926
FILING DATE: 19-JUN-1996
CLASSIFICATION: 435
ATTONREY/AGENT INPORMATION:
NAME: RODERT J. CODERT
REGISTRATION NUMBER: 36,108
REPRENCE/POCKET NUMBER: 36,108
REPRENCE/POCKET NUMBER: 36,108
TELEPRAK: (914) 345-7400
TELEPRAK: (914) 345-7213
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2282 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-088-187A-11 (1-341) x US-08-665-926-5 (1-2282)
US-08-665-926-5
; Sequence 5, Application US/08665926
; Patent No. 5851797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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37.55%
23.67%
5.79%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
357..1847
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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1371 TGGAAAGAATATAAAGTGGGATTTGGTAACCCTTCAGGAGAATATTGGCTGGGAAATGAG 1430
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TTTGTTTCGCAACTGACTAATCAGCAACGCTATGTGCTTAAAATACACCTTAAAGACTGG 1490
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| 1731 TACTATCCACAGAGGAGAAAAAAAAAAAAAACGGCATTAAATGGTACTACTACGGAAA 1790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 Tyr-----HisSerThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAlaArg 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 SerValTyr------ProGluSe 147
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58
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Matches:
Conservative:
Mismatches:
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APPLICATION NUMBER: US 08/319,932
            FILING DATE: 07-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
                                                                                           REFERENCE/DOCKET NUMBER: R
TELECOMMUNICATION INFORMATION
TELEPHONE: (914) 345-7400
                                                                                                                                TELEPHONE: (914) 345-7400
TELEPAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 2282 base pairs
                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            104.00
37.55
23.67
5.79
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                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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357..1847
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Best Local Similarity:
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LOCATION:
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                                       1671 CAAATGCTAACAGGAGGCTGGTGTTTGATGCATGTGGTCCTTCCAACTTGAACGGAATG 1730
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                                                                                                                                                                                                                                                           -----LysileProLysLy 182
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                                                                                                                                                                                                                                                                                                                                     182 sArgGlyArgLysLysLysAsnAlaAspProGluGluIleAsnSerSerAlaProArgAs
                  ------ValllePheProSer
                                                                                                                                                                                                                                                                                              1791 GGCTCAGGCTATTCGCTCAAGGCCACAACCATGATGATCCGACCAGCAGATT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT:
DAVIS, et al.
TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                       167 oValLysAlaGluGluProThrProThrPro----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B: Regeneron Pharmaceuticals, Inc
777 Old Saw Mill River Road
              122 LeuPheGluAspLeuGluAspGluAspAlaGlu-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZUP. 10:591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PSTEM: PC-DOS/MS-DOS
SOFTWARE: PSTEDIIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFFLLOW DATE: 09-DEC-122.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
TTTMC DATE: 02-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLING DATE: 02-DEC-1.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/373,579
PILING DATE: 17-2AN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 05-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/418,595
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09162437
Patent No. 6166185
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1893 CTTAAGCCCAGTGCAC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1992 AGAGCCTGTAAAC 2004
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STATE: New York
COUNTRY: USA
                                                                                           138 SerValTyr-
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TYPE: DNA
ORGANISM: Artificial Sequence
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US-08-817-318-5
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US-08-817-318-5
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                                               .893 CTTAAGCCCAGTGCAC------------TGAAAGTCACGGCTGCGCACTGT 1931
                          ---AlaAlaLysThrPh 237
                                                                                                                                                      Sequence 5, Application US/08740223A
Patent No. 6265564
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: Expressed Ligand - Vascular
TITLE OF INVENTION: Intercellular Signalling Molecule
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2282
58
34
92
61
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LOCATION: 1...2282
OTHER INFORMATION: from clone pBluescript KS
OTHER INFORMATION: encoding human TIE 2 ligand
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                              E: Regeneron Pharmaceuticals, Inc 777 Old Saw Mill Road
                            lThralaGluGluArgGluArgAlaIleAsn---
                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,223A
FILING DATE: 25-OCT-1996
CLASSIPICATION: 536
PAPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Cobert, Robert J
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 333
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7721
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Coding Sequence
LOCATION: 357...1844
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
                                                                                                     1992 AGAGCCTGTAAAC 2004
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                                                                                   237 eGluProThrAgn 241
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
                                                                                                                                                                                                                                                                                                       CITY: Tarrytown
STATE: NY
COUNTRY: USA
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Best Local Similarity:
Query Match:
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1791 GGCTCAGGCTATTCGCTCAAGGCCACAACCATGATGATCCGACCAGCAGATT----- 1842
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| Inctaticcacagaggcagaacacaaataagticaacggcattaaatggtactactggaaa 1790
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1932 GTCCTCTTCCACCACAGAGGGCGTGTGCTCGGTGCTGACGGGACCCACATGCTCCAGATT 1991
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| :::||| :::||| :::||| :::||| :::|| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::|
1371 TGGAAGAATATAAAGTGGGATTTGGTAACCCTTCAGGAGAATATTGGCTGGGAAATGAG 1430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sArgGlyArgLysLysAsnAlaAspProGluGlulleAsnSerSerAlaProArgAs 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 rThrValProAlaAsnLysGlyTyrAlaSerSerAlaIleGlnThrLeuPheThrGlyPr 167
                                                                                                                                                                                                                                                                                                                                                                                                           104 Tyr-----HisSerThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAlaArg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 LeuPheGluAspLeuGluAspGluAspAlaGlu------ValllePheProSer 137
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                                                                                                                                                                                                                                 -----IlePheArgTyr
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TITLE OF INVENTION: TIE-2 LIGANDS, METHODS OF MAKING AND USES THEREOF FILE REFERENCE: REG 330-F-PCT-US
CURRENT APPLICATION NUMBER: US/08/817,318
CURRENT FILING DATE: 1999-09-16
NUMBER OF SEC ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
                                                                                                                                                                                           Pheval AspArgTyrSerIleArgIleGlyTyrLeuLeu-
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OTHER INFORMATION: Unknown Organism
NAME/KEY: CDS (1947)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 5, Application US/08817318 ; Patent No. 6433143
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1371 TGGAAAGAATATAAAGTGGGATTTGGTAACCCTTCAGGAGAATATTGGCTGGGAAATGAG 1430
                                                                                                                                                                                                                                                                                  1551 TATAGGATTCACCTTAAAGGACTTACAGGGACAGCCGGCAAAATAAGCAGCATCAGCCAA 1610
                                                                                                                                                                                                                                                                                                                                                                                                        1671 CAPATGCTAACAGGAGGCTGGTGTTTGATGCATGTGGTCCTTCCAACTTGAACGGAATG 1730
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| 1731 TACTATCCACAGAGGCAGAACACAAATAAGTTCAACGGCATTAAATGGTACTACTGGAAA 1790
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1791 GGCTCAGGCTATTCGCTCAAGCCACAACCATGATGATCCGACCAGCAGATT----- 1842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 Tyr-----HisSerThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAlaArg 121
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                                                                                                                                                                                65 TrpGln-----Glu 67
                                                                                                                            45 GlyHisValTrpArgValGlyLeuArgLysAlaAspAsnLysIleTrpPheGlnAspGly 64
                                                                                                                                                                                                                                  PhevalAspArgTyrSerIleArgIleGlyTyrLeuLeu------IlePheArgTyr 84
          2282
58
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            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                    US-10-088-187A-11 (1-341) x US-08-817-318-5 (1-2282)
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            0.0266
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Query Match:
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Alignment Scores:
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Sequence 1318, Application US/10767795

Publication No. US20040181830A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Shou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REPERENCE: 38-21(53534)B
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQ ID NO 1318
                                                             US-09-938-842A-273
US-09-938-842A-273
US-09-938-842A-273
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US-09-938-842A-273
US-09-938-842A-273
US-10-424-599-118105
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US-10-437-963-11818181
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ORGANISM: Gossypium hirsutum
FEATURE:
                        Length
                                                                                           RESULT 1
US-10-767-795-1318
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165.5
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246
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Result
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-LONDLOG -DEV TIMEOŪT=120 -WANT TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                      December 30, 2004, 06:32:43 ; Search time 1535 Seconds (without alignments) 1254.759 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                     MPRPFFHKLIFSSTIQEKRL.....LLRTRDFVLKVTAFRVNEYV 341
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20: /cgn2_6/ptodata/1/pubpna/USO0P_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/USO0P_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/USO0P_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/USO0P_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/USO0P_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/USO0P_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/USO0P_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/USO0P_PUBCOMB.seq:*
                   GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                 - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Xgapop 10.0 ,
Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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Database :

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Total number

Searched:

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Sequence 2973, Ap Sequence 64127, A Sequence 64127, A Sequence 130216, Sequence 35166, A Sequence 35166, A Sequence 36556, A Sequence 60237, A Sequence 60237, A Sequence 14762, A Sequence 74762, A Sequence 1451, Ap Sequence 3941, Ap Sequence 3451, Ap Sequence 36606, A Sequence 3451, Ap Sequence 36606, A Sequence 36606, A Sequence 36606, A Sequence 36606, A Sequence 36606, A Sequence 36606, A Sequence 36606, A Sequence 36606, A Sequence 36606, A Sequence 36606, A Sequence 36606, A Sequence 36606, A Sequence 36606, A Sequence 36606, A

Sequence 312, App Sequence 89684, A

, OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C1540_1 US-10-767-795-1318

SUMMARIES

Sequence 237, App Sequence 37591, A Sequence 3743, Ap Sequence 3743, Ap Sequence 38685, A Sequence 38631, A Sequence 32044, A Sequence 75700, A Sequence 75700, A

Sequence 1316, Ap Sequence 97592, A Sequence 1317, Ap Sequence 9015, Ap

Sequence 273, App Sequence 118105, Sequence 1318, Ap

Sequence 75700, A Sequence 23571, A Sequence 7926, Ap Sequence 107372, Sequence 101386, Sequence 49771, A

Sequence 2973, Ap

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ArgsertyspheryrGluseralaserAlaArgFysArgThrValThrAlaGluGluArg 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1252 ACCGTATTTCGTGTAATGGAA 1272
                                                                ThralaPheArgValAsnGlu 339
                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Arabidopsis thaliana
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946.00
87.18%
81.20%
52.67%
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Best Local Similarity:
Query Match:
DB:
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US-09-938-842A-273
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Pred. No.:
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                                                                                                                                                                      ThrValProAspGlyHisValTrpArgValGlyLeuArgLysAlaAspAsnLysIleTrp
                                                                                                                                                     202 AIGCCACGCCCTTTTTCCATAAGCTTATTCTCTCCACTACTCTCCAGGACAGGAAACTG
                                                                          1 MetProArgProPhePheHisLysLeuIlePheSerSerThrIleGlnGluLysArgLeu
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     1471
222
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63
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                                                           US-10-088-187A-11 (1-341) x US-10-767-795-1318 (1-1471)
      Length:
Matches:
Conservative:
Mismatches:
Indels:
    2.14e-127
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72.48%
60.49%
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Best Local Similarity:
Query Match:
DB:
Alignment Scores:
Pred. No.:
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Sequence 273, Application US/09938842A

Sequence 273, Application US/09938842A

Sequence 274, Application US/09938842A

Sequence 275, Application US/09938842A

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REPERENCE: SCRIP1300-3

CURRENT FILING DATE: 2001-08-24

PRIOR PPLICATION NUMBER: US 60/227,866

PRIOR PPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR PILING DATE: 2000-08-24

PRIOR PILING DATE: 2000-06-24

PRIOR PILING DATE: 2000-01-01-16

PRIOR FILING DATE: 2001-01-16-22

NUMBER OF SEQ ID NOS: 5379

LENGTH: 681
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                                    312
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Sequence 118105, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLS REPERENCE: 38-21(5323)B
CURRENT APPLICATION UNDRER: US/10/424,599
CURRENT PILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 118105
                                                                                                                                                                                                                                                                      LeuargProSerTyrLeuTyrArgGlyCysIleMetTyrLeuProSerGlyPhealaGlu 267
 GAACCAGTGAATAAAGGTTATGGCGGTTCTACAGCCATCCAAAGCTTTTTCAAA---GAA 165
                                          166 TCTAAAGCTGAAGAA-----ACGCCCAAGGTACTTAAGAAGAAGAAGAAGAAGAAG 216
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                                                                                                                                                 ArgSerLyBPheTyrGluSerAlaSerAlaArgLyBArgThrValThrAlaGluGluArg
                                                                                        LysAsnAlaAspProGluGluIleAsnSerSerAlaProArgAspAspAspProGluAsn
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                             VallysAlaGluGluProThrProThrProLysIleProLysLysArgGlyArgLysLys
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Fublication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Court STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR SEQ ID NOS: 5379
SEQ ID NO 273
TUNGER OF SEQ ID NOS: 5379
TUNGER OF SEQ ID NOS: 5379
TUNGER OF SEQ ID NOS: 5379
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 277 CGCTCAAAGTTCTACGAGAGTGCTTCTGCTAGAAAGAGAACTGTAACTGCAGAGGAAAGA 336
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US-09-938-842A-273
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'n	20 LeuargvalproagpLysPhevalSerLysPheLysAspGluLeuSerValAlavalAla 39        ::           :::     :::	40 LeuthrvalproaspdlyHisvalTrpargValGlyLeuArgLysAlaAspAsnLysIle 59    :::	60 TrpPheGlnAspGlyTrpGlnGluPheValAspArgTyrSerIleArgIleGlyTyrLeu 79 	80 LeuilePheArgTyrGluGlyAsnSerAlaPheSerValTyrIlePheAsnLeuSerHis 99 :::	100 SerGlulleAsnTyTHiSSerThrGlyLeuMetAspSerAlaHisAsnHisPheLysArg 119 	120 AlaArgLeuPheGluAspLeuGluAspGluAspAlaGluValIIePhe 135 :::       :::::          :: 812 TGTCTTAAATTTTTTGAAGAAATGGAAGGTGAAGATTCCATTGAAATCTCGGATTCATCA 871	136 ProserserValTyrProSerProLeuPro	148 ThrvalproalaasnLysGlyTyralaSerSeralaileGlnThrLeuPheThrGly 166 	166 166	992 AAACTTAATAGCATAAACTGGGGAGAAGGTGGTAATGCCCATTCTTCAAGAAGTGCCAAT 1051	167	172 GluProThrProThrProLyBIle	185	205 ProgludenargSerLysPheTyrGluSerAlaSerAladrgLysArgThrValThrAla 224 	225 GlugluarggluargalaileabanalaalaiysThrpheGluproThrasnProPhePhe 244 	245 ArgValValLeuArgProSerTyrLeuTyrArgGlyCysIleWetTyrLeuBroSerGly 264 	265 PheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysValGlnLeuAlaGlu 283 	284 LysGlnTrpProValArgCysLeuTyrLysAlaGlyArgAlaLysPheSerGlnGlyTrp 303 :::	304 TyrglupherhrLeugluhsnasnieuglygluglyaspvalcysvalphegluLeuleu 323 :::       :::

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Quence 1316, Application US/10767795

Quence 1316, Application US/20040181830A1

WERAL INFORMATION:

PPLICANT: Kovalic, David K.

PPLICANT: Cao, Yongwei

PPLICANT: Cao, Yongwei

TILE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TILE OF INVENTION: Plants and Uses Thereof For Plant Improvement

ILE REFERENCE: 38-21(55534)B

RRENT APPLICATION NUMBER: US/10/767,795

RRENT FILING DATE: 2004-01-30

PHERO PS SEQ ID NOS: 117596

1 ID NO 1316
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Matches:
Conservative:
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Oy 172 uProThrProThrProLys1leProLysLysArgGlyArgLysLysLysAsanAlaAspPr 192	Oy 192 oGludlulleAsnSerSerAlaProArgAspAspProGluAsnArgSerLysPheTy 212	Oy 212 rGluSerAlaSerAlaArgLysArgThrValThrAlaGluGluArgGluArgAlaIleAs 232 	Qy 232 nAlaAlaLysThrPheGluProThrAsnProPheArgValValLeuArgProSerTy 252	Oy 252 rLeuTyrArgGlyCygIleMetTyrLeuProSerGlyPheAlaGluLygTyrLeuSerGl 272 	Qy 272 ylleSerGlyPheIleLysValGlnLeuAlaGluLysGlnTrpProValArgCysLe 291	Qy         291 uTyrLysAlaGlyArgAlaLysPheSerGlnGlyTrpTyrGluPheThrLeuGluAsn 310                 :::	RESULT 6 US-10-424-599-97592 ; Sequence 97592, Application US/10424599	; Publication No. US20040031072A1 ; GENERAL INFORMATION; ; APPLICANT: La ROGA Thomas J ; APPLICANT: Kovalic David K	; APPLICANT: Zhou Yinua ; APPLICANT: Cao Yongwei ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement	,	; SEQ IN NO 97592 ; TYPE: DNA ; ORGANISM: Glycine max	; CTHENTEL INFORMATION: Clone ID: PAT_MRT3847_59139C.1 US-10-424-599-97592	1.43e-95 Length: 835.50 Matches: 58.81% Conservat	Mismatches: Indels: Gaps:	-10-088-187A	182 ATGCCTTGCCCTTGTTTCCTCAAGCTTGCTATCACTCTCAATCTACATACCTGATCACT 20 uArgValProAspLysPheValSerLysPheLysAspGluLeuSerValAlaValAlaLe 1    :::	Db 242 GAGGAITCCAGAIAAITITCTGAGGAAAIAIGGGACCCAGCITICTACAAITGCTACCT 301  Qy 40 uThiValProAspGlyHisValTrpArgValGlyLeuArgLysAlaAspAshLysIleTr 60	302 CACIGIICCIGAIGGIAGIGIIIGGCGIAIAGAAIIGAAAAAAAA

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Percent Similarity:
Best Local Similarity:
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US-10-021-323-9015
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Sequence 1317, Application US/10767795
Sequence 1317, Application US/10767795
Sequence 1317, Application VG20040181830A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihuwa
APPLICANT: Zhou, Yihuwa
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53534)B
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQ ID NO 1317
LENGTH: 1062
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Matches:
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Mismatches:
Indels:
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82.49%
74.01%
35.63%
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Query Match:
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US-10-021-323-9015
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LOCATION: (1)..(644)
OTHER INPORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3828-022-Q1-K6-E11
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Matches:
Conservative:
Mismatches:
Indels:
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
; LENGTH: 644
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ORGANISM: Gossypium hirsutum
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Sequence 97591, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
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                                                                                                                   TyrGluPheThrLeuGluAsnAsnLeuGlyGluGlyAspValCysValPheGluLeuLeu
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_59138C.1
US-10-424-599-97591
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US-10-767-795-1320
Sequence 1320, Application US/10767795
Publication No. US20040181830A1
GENERAL INFORMATION:
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68.52%
20.91%
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                           APPLICANT: Rameera, Joshua G.
APPLICANT: Rameera, Joshua G.
APPLICANT: Matthew, Abraham V.
APPLICANT: Matthew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Woesener, Jeffrey P.
APPLICANT: Made, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Kricker, Maja
APPLICANT: Slader, Ted
APPLICANT: Allen, Keith R.
APPLICANT: Allen, Keith R.
APPLICANT: Allen, Keith R.
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Lialiana
FILE REFERENCE: 2028 (PARA-017RV)
CURRENT ALING DATE: 2020 (PARA-017RV)
CURRENT ALLING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SEQ ID NO 237
LENGTH: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                  604 ATACCGGGGATGTATTATGTACTTACCATCA 634
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Publication No. US20020040490A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
APPLICANT: Hamilton, Carol M.
APPLICANT: Raines, Tracy M.
APPLICANT: Raines, Tracy M.
APPLICANT: Raines, Joshua G.
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COCATION: (1)...(426)
COTHER INFORMATION: n = A.T.C or
US-09-770-423-237
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US-09-770-423-237/c
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Sequence 3743, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Show, Yihue
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: 18-21/335.34 US
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQ ID NO 1320
LENGTH: 650
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Matches:
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Best Local Similarity:
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US-10-739-930-3743/c
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1367 AAGAGAAAAGTTAACTCAGTTGATTTCTTCAACAATGTCAAATGAGAAGTCGCAAGTGT 1308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 GlyProValLysAlaGluGluProThrProThrProLysIleProLysLysArgGlyArg 185
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Matches:
Conservative:
Mismatches:
Indels:
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OTHER INFORMATION: unsure at all n locations
CURRENT FILING DATE: 2003-12-18
WHDER OF SEQ ID NOS: 11088
SEQ ID NO 3743
LENGTH: 2207
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329.00
43.77%
27.25%
18.32%
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ORGANISM: Glycine m
PEATURE:
NAME/KEY: unsure
LOCATION: (1)..(220
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Best Local Similarity:
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|1391 AAAGCTGGTAAAAGGAGGCCTCAAGCTGCCACTTCAAAGGATGTGGTCGATGATTGTTCAC 1450
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TCCCAAAGGCGCCGAGTAACCGAAGAAGAGAAGTGCCTTGCTCTCAGAAAGGCAATGGAG 1630
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                                                                                                                                                                                               GATGGAGGAGCGACGAGGAGAACAGGAGCGACGAGTGGTGGTGGCGCTGGCGGCGCCCTCT
                                                                                                                                          1091 AcceccaAcceccecceccercAAccrcaAdaceccAAGCCGACGACGCCTCCGAGGG
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|TICAAGTCGAAGCACCCTTCACCATGCAGATAATGATCGAGTCTTATGTCTACGTGGGA
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                                               100 SerGluIleAsnTyrHisSerThrGlyLeuMetAspSerAla-------
114 ---HisAsnHisPheLysArgAlaArgLeuPheGlu-
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; Publication No. US20040123343A1
; RENEAL INFORMATION:
APPLICANT: LA ROBA, Thomas J.
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Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Co, Yonguic, Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APLICATION NUMBER: 2010/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
   |||:::
TTCAAATCTTGTAATCCATTCTTGACGGTCATGCAACCCACATCAGTTCTCAC 1128
                                                                                                                           1127 GGTAGTCTGAACTTACCAATGAAGTTCTGAAGAGTCACCTTGATTTGCACAAGAAGCGG 1068
                                                                                                         GlyPhelleLysValGln---LeuAlaGluLysGlnTrpProValArgCys---LeuTyr 292
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                                            257 CyslleMetTyrLeuProSerGlyPheAlaGluLysTyrLeuSer-----GlylleSer 274
                                                                                                                                                                      LysAlaGlyArgAla---LysPheSerGlnGlyTrpTyrGluPheThrLeuGluAsnAsn 311
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Matches:
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Mismatches:
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Query Match:
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US-10-425-115-89685
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LENGTH: 2338
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 32044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 AGGCGTCCGGTAACTGAAGCAGAAGGACCATGCTCTTCAAAGGGCAAGAAGTTTAAA 659
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 836
                                                                      779
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395 AAGGTAACATCGACAAGCCATAACAGTACCAGAGGTTCATCATGCAGCTCAGATGAAGAT
                                                                                                                                 :::|||
GTGTCTCGGGGTGGTAGATGTGTTTCAAAGGGTCAAAGACAACTAACAGTAATATCACAG
                                                                                                                                                                                                                                                                                                            MetTyrLeuProSerGlyPheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLys
                                                                                                                                                                                                                                                                                                                                                                                279 ValGlnLeuAlaGlu---LysGlnTrpProvalArgCysLeuTyrLysAlaGlyArgAla
                                   196 AsnserserAlaProArgAspAspAspProGluAsnArgSerLysPheTyrGluSerAla
                                                                LysArgThrValThrAlaGluGluArgGluArgAlaIleAsnAlaAlaAlaLysThrPheGlu
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                                                                                                           216 SerAlaArg------
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OTHER INFORMATION:
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Best Local Similarity:
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTGACAAGATATCAACT-----TTCTCTGCTCACCCT----TCCAAAATGTG 1118
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        Kovalic, David K
Zhou, Yihua
Cao, Yongwei
Wu, Wei
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237 CACCTGAAATCACCTAGCAGCGCTGAGACATGGCACGTCGGTGTAGAGAAGCATGGCGAC 296
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To (bases 1 to 1307)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' CDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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CD813712
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AV539103
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-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10088187/runat_29122004_115842_127/app_query.fasta_1.519
-D=/cgn2_1/USPTO_spool/US10088187/runat_29122004_115842_127/app_query.fasta_1.519
-DB=SET -QPMT=fastap -SUPFIX=ree -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15. -MODE=LOCAL
-OUTFWT=pcc -NORM=ext -HRAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10088187_@CGN 11 3437_@runat_29122004_115842_127 -NCPU=6 -ICPU=3
-UN MAMP -LAARGEQUERY -NGS_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THRADS=1 -XGAPEPP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DBLEXT=7
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               GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
                                                                                       nucleic search, using frame_plus_p2n model
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Database :

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Score

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HTC 06-FEB-2004

from clone

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BX823300.1 GI:42464860
HTC; GSLT_CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophya; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 1441)
S Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Craud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
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Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

MROV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

Http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full length
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Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTLS20ZG12 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).
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                                                                                            AsnProPhePheArgValValLeuArgProSerTyrLeuTyrArgGlyCysIleMetTyr
                                                                                                                                                                                                                                                                                    LeuProSerGlyPheAlaGluLy8TyrLeuSerGlyIleSerGlyPheIleLy8ValGln
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URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Wunich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
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Arabidopsis thaliana Full-length CDNA Complete sequence from clone GSLTFGH542804 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).

BX824523.

BX824523.

GSLTCDNA.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana (thale cress)

EWATOTOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Streptophyta; Magnoliophyta; Gastelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.

Mhole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGY INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Wunich Information center for Protein Sequences) . 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Erjetll_length
                                                                                                                                                                                                                                           LeuProSerGlyPheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysValGln
                                                                                                                                                              GlnGlyTrpTyrGluPheThrLeuGluAsnAsnLeuGlyGluGlyAspValCysValPhe
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                                             1011 CTTCCTTCTGGGTTTGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAAGTCCAG
                                                                                                           LeualaGluLysGlnTrpProValArgCysLeuTyrLysAlaGlyArgAlaLysPheSer
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Useroscope.

Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EWRX cedex - FRANCE (B-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

NRGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences) 5 prime and 3 prime are assembled with Phrap.
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BX816536
BX816536
BX816536
BX816536.1 GI:42473594
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 1346)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' CDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                     CNSOAD6P 1346 bp mRNA linear HTC 06-FEB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH54ZB06 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).
321 GluLeuLeuArgThrArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyr
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Conservative:
Mismatches:
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Best Local Similarity:
Query Match:
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CK120978 1 GI:47831294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 780)
Feilner, T., Immink, R.G.H., Cahill, D.J. and Kersten, B.
Generation of a cDNA expression library from Arabidopsis
inflorescence meristem
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                   785
                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/ecotype="columbia"
/ecotype="Columbia"
/db_xref="dAB1:952488"
/db_xref="taxon:3702"
/clone="WRWGp2011014204"
/tissue_type="Inflorescence meristem"
/dev_stage="about one week after bolting"
/lab_host="E. coli SCS-1/pSE111"
/clone=lb="AtM1"
/note="Vector: pQE-30NAST-attB (AY386205); Site_1: SalI;
Site_2: Not1; About 1 week after bolting, cDNA synthesis
                                                                    243
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                                                 pAspProGluAsnArgSerLysPheTyrGluSerAlaSerAlaArgLysArgThrValTh 223
                                                                                                                                                                                       erGlyPheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysValGlnLeuAlaG
                                                                                                                                                                                                                                                                                                                               lulyaGlnTrpProValArgCysLeuTyrLyaAlaGlyArgAlaLysPheSerGlnGlyT
                                                                                                                                                                                                                                                                                                                                                 rAla-GluGluArgGluArgAlaIleAsnAlaAlaLysThrPheGluProThrAsnProP
                                                                                                                                         euArgThrArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyrVal 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAGAACTCGGGATTTCGTTCTCGAAGTCACCGCCTTTCGTGTCAAGAGTATGTG 841
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Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Inhestr. 3, D-14195 Berlin, Germany
Tel: +49(0)30/8413128
Fax: +49(0)30/84131128
Email: Kersten@molgen.mpg.de
Insert Length: 780 Std Error: 0.00
Plate: 204 row: 0 column: 14
Seq primer: pQE65,
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1. .780
/organism="Arabidopsis thaliana"
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CK120978
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using SuperscriptTM-system (Invitrogen) with an oligo(dT)-primer containing NoII restriction site and a sall adapter. The main library (plate numbers begin with 1) of 38,000 clones was rearrayed into the sublibrary (plate numbers begin with 201) containing 5,000 putative expression clones. Average Insert size is 1 Kb. Note: The containing clones in the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing stream of the containing strea
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ORIGIN		Tank / / : ad	}
Alignment S Pred. No.: Score: Percent Sim: Best Local is Query Match DB:	cores: ilarit Simila	1.12e-98 1016.50 1016.50 83.09\$ irity: 75.90\$	Length: 780 Matches: 211 Conservative: 20 Mismarches: 21 Indels: 26 Gaps: 9
US-10-0	88-187A-11	1 (1-341) x CK120978 (1	(-780)
ò		8AlaAspAsnLysIleTrpPheGlnAsp(     :::	GlyTrpGlnGluPheValAspArgTyrSer
පු	2 AAA	<b>AGCCAACAACAAATCTGGTTTC</b>	AAGACGGTTGGCAGGAGTTTGTCAACCGTTTCTCC 61
oy Og	74 Ile     62 ATT		ePheArgTyrGluGlyAgnSerAlaPheSerValTyr 93             -TTGGGAIACAAAGTTACAGTCTAC 97
à	94 Ile	ePheAsnLeuSer-HisSer	
q	98 ATT	TTCAATTTATCCTCCACACTCT	rgagatcaaccaccattctagtagtgaagctcttat 157
ć	109 -Le	euMetAspSerAlaHisAsnHis	-LeuMetAspSerAlaHisAsnHisPheLysArgAlaArgLeuPheGluAspLeuGl 127
qq	158 GCA	AAATGGATTCCGCACAGAATCAG	strcaacaaacgrecrcaatrgitrgaagaiccrga 217
ò		spGluAspAlaGluValIlePhe	14
<b>q</b>		TCAAAGATGCTAAGGTCATTTA1	25
δ	147 rTh	hrValProAlaAsnLysGlyTy1	rThrValProAlaAgnLygGlyTyrAlaSerSerAlaIleGlnThrLeuPheThrGl 166
ф	260 TAC	crgaaccagrgaaraaaggrrar	rggcggttctacagccatccaaagctttttcaaa 317
È	166 yPr	roValLysAlaGluGluProTh1 	yProvallysAlaGluGluProThrProThrProLysIleProLysLySArgGlyArgLy 186
q	318 -GA	aatctaagctgaagaa	ACGCCCAAGGTACTTAAGAAGAGGAAGGAA 367
ò		ysLysAsnAlaAspProGluGlu	0 0
ορ	368 GA	agaagaatcctaatcccgaggai	42
à	206 uAs	snArgSerLysPheTyrGluSe	uasnargserlysphefyrgluseralaseralaarglysargfhrValfhralaglugl 226
QΩ	428 GAP	accecrcaaagrrcraceagag:	igcircigciagaaagaacigiaacigcagaga 487
ò	226 uAr	rgGluArgAlaIleAsnAlaAla	₹*
QQ	488 AAC	gagagagagagagagagagaga	caaaacatrogaaccaacaaarcctractragagr 547
ò	246 1Va	alLeuArgProSerTyrLeuTy:	1 26
ф	548 TG	trcreceaccarcararctara	9
ò	266 aG	luLysTyrLeuSerGly1leSe	aglulysTyrLeuSerGly11eSerGlyPhe11eLysValGlnLeuAlaGluLysGlnTr 286
ф	608 TG	AGAAATACCTAAGTGGGATATC	rddiricarcaadcrecagereagaaacaarg 667
ò	286 pP	roValArgCysLeuTyrLysAl	0
q	) 100 100 100 100 100 100 100 100 100 10	cagraderecerciacaaaec	agggagaggtaagtttaggccaaggatggtatgagtt 727

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701 bp mRNA linear EST 10-JUL-2003
Brassica napus cDNA clone BN25045C06, mRNA
                                                                                                                                                                                    358
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Brassica napus (rape)

Brassica napus

Brassica napus

Brassica napus

Brassica viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Sparmarophyta; Magnoliophyta; eudicotyledons; core eudicots;

Sparmarophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

I (bases 1 to 701)
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                                                                                                                                                                                                                                                                                                       359 GATGAATGCATCTCTCCAGCACTTCAGAATTTGTTTGGTGGGTCTAAACTTAACAACTGC 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaargiysargThrValThrAlaGluGluArgGluArgAlaIleAsnAlaAlaLysThr 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256
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Tel: 33 1 69 47 54 10
Tel: 13 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
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                                                                                                                                                           242 GCTTTCAGTGTTAGTATATTTAATTTGTACAACTCGGAAATAAACTATCAGACTAATGCC
                                                                                                                                                                                                                                               GluAspAla------GluValIlePheProSerSerValTyrProSerPro
                                                                                                                                                                                                                                                                                                                                                                        144 Leu------ProGluSerThrValProAlaAsnLysGlyTyrAlaSerSerAlaile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTGAGCCAACTAACCCTTTCTGCAGGTCGTCTTGCGACCATCTTATCTGTACAGGGGA
                                                                                                                            LeuMetAspSerAlaHisAsnHisPheLysArgAlaArgLeuPheGluAspLeuGluAsp
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Eb Gossypium raimondii cDNA clone GR_Eb0039N17
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 906)
1 (Km.H., Yu.Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
Udall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and
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Unpublished (2004)
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
The University of Arizona
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3', mRNA sequence.
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction: Temple G.
Genoscope members carried out sequencing and annotation: Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGY INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
          Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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1 (Bases I to 1041)
Castelli, V. Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J., and Salanoubst, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 Phe-------GluAspLeuGluAspGluAspAlaGluValllePheProSerSer 138
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http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=ArabidopBis.
Location/Qualifiers
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Mismatches:
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BX835682 Arabidopsis thaliana Adult vegetative tissue Col-0
Arabidopsis thaliana cDNA clone GSLTLS48ZH11 3PRIM, mRNA sequence.
BX835682.1 GI:42529765
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932.00
92.12%
88.67%
51.89%
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Percent Similarity:
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us-10-088-187a-11.rst

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CD823066 645 bp mRNA linear EST 10-JUL-2003 BN25.047120F020109 BN25 Brassica napus CDNA clone BN25047120, mRNA sequence.
CD823066.1 GI:32505006
                                                                                                                                                        243
                                                                                                                                                                                                                                                                                                                                         Brassica napus
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, rosids, eurosids il Brassicales, Brassicaceae; Brassica.

1 (bases 1 to 645)
Genoplante.
                                                                                                   380
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                                                                                                                                                                                                                                                                                           144 uProGluSerThrValProAlaAsnLysGlyTyrAlaSerSerAla---IleGlnThrLe 163
                                                                 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
                                                                                                                                                                                                                           223 rAlaGluGluArgGluArgAlaIleAsnAlaAlaLysThrPheGluProThrAsnProPh
                                                                                     gglyArgLysLysAsnAlaAspProGluGluIleAsnSerSerAlaProArgAspAs
                                                                                                                                                                                                      203 pAspProGluAsnArgSerLysPheTyrGluSerAlaSerAlaArgLysArgThrValTh
                        274 -CCTGAATCTACTGAACCAGTGAATAAAGGTTATGGCGGTTCTACAGACATCCAAAGGTT
                                                                   163 uPheThrGlyProVallysAlaGluGluProThrProThrProLysIleProLysLysAr
                                                                                                                                                                                                                                                                                                                                                                                                          93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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Mismatches:
Indels:
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/db_xref="taxon:3708"
/clone="MRS5047L20"
/tissue type="geed"
/clone_lib="BN25"
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786.00
98.70%
96.75%
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DB:
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                                                                                                                 Arabidopsis thaliana (Unale Cress)
Arabidopsis thaliana (Unale Cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 669)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Cono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Diarge scale analysis of Arabidopsis full-length cDNA (2002b)
Contact: Motoaki Seki
Diarge scale canalysis of Arabidopsis full-length cDNA (2002b)
Trel: 81-298-36-9160
Email: Motoaki Sciences Center
3-1-1 Koyadai, Tshkuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9160
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length CDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a Stl/Xhol insert. Please visit our further details.

Further details.
     AV821829 AFL4 Arabidopsis thaliana cDNA clone RAFL04-16-P22 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 ------LeuMetAspSerAlaHisAsnHisPhe---LysArgAlaArgLeuPheGl 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 ServalTyrIlePheAsnLeu---Ser-HisSerGluIleAsnTyrHisSerThrGly-- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 AGCTCTTATGCAAATGGATTCCGCACAGAATCAGTTCAACAAACGTGCTCGATTGTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="RAFL4"
/note="Site 1: Sst1; Site 2: XhoI; subjected to
cold-treated(1,2,5,10,24 hr)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         669
171
18
22
26
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                        Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                      mRNA sequence.
AV821829
AV821829.1 GI:19863860
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789.50
79.75%
72.15%
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AUTHORS
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Alignment Scores: Alignment Scores: Pred. No.: Score: Precent Similarity: Best Local Similarity: Coury Match: 71.50 Matches: Percent Similarity: F57.19\$ Mismatches: A2.96\$ Indels: Cousery Match: 7 Gaps: 7 US-10-088-187A-11 (1-341) x CO094348 (1-834)	Oy 67 GluPheValAspArgTyrSerIleArgIleGlyTyrLeuLeuIlePheArgTyrGluGly 86	107 ThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAlaArgLeuPheGluAspLeu 12.  123 AATGCTTCTTGTAGTCAATACAATCATGGGAATCATATCGTTCGATGAACGATGAACGATGAACGATGAACGATGAACGATGAACGATGAACGATGAACGATGAACGATGAACGATGAACGATGAACGATGAACGATGAACGATGATGAACGATGATGATGAACGATGATGATGATGATGAACGATGATGATGATGATGATGATGATGATGATGATGATGATG	Oy 147 SerThrValProAlaAsnLysGlyTyrAlaSerSerAlaIleGlnThrLeuPheThrGly 166	0y 166
Qy       185 ArgLysLysLysBanAlaAspProGluGluIleAsnSerSerAlaProArgAspAsp 204         Db       3 AGGAGAAGAAGAACCTGTTCTGAGGAAGTAACTCTTCTCTCTGAGGATGATGACG 62         Qy       205 ProGluAsnArgSerLysPheTyrGluSerAlaSerAlaArgLysArgThrValThrAla 224         Db       63 CCGGAGAGCCGTTCAAAGTTCTACGAGAGGACGGTTACTGCA         Qy       225 GluGluArgGluArgAlaIleAsnAlaAlaLysThrPheGluProThrAsnProPhePhe 244         Db       123 GAGGAAAGAGAGGCCATTAATGCAGCCAAAACGTTCGAGCACAACAAACCCTTTCTTC 182	Oy 245 ArgValValLeuArgProSerTyrLeuTyrArgGlyCysileMetTyrLeuBroSerGly 264	285 GlnTrpProValArgCysLeuTyrLysAladlyArgAlaLysPheSerGlnGlyTrpTyr	<pre>Qy 325 ThraxgAspPheValleuLysValThralaPheArgValAsn 338                                      </pre>	RESULT 15 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C009444 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C0094348 C009448 C009448 C009448 C009448 C009448 C009448 C009448 C009448 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C00948 C009

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GHVWRVGLRKADNKIWPQDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEI
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QTLFTGPVKABEPTPTPKI PKKRGRKKKNADPEEINSSAPRDDPERRSKFYESASAR
KRTYABERREAINAKTFEPTNPFFRVVLRPSYLYRGCIMTLPSGPAKKYLSGISGF
IKVQLABEKQMPVRCLYKAGRAKFSQGMYEFTLENNLGEGDVCVFELLRTRDFVLKVTA
FRVNEYV"
                                                                                AC145449 Medicago
AY661659 Sorghum b
AC097280 Oryza sat
AL954829 Oryza sat
AF164919 Arabidops
AC07504 Arabidops
AC07504 Arabidops
AC075044 Arabidops
AJ526944 Arabidops
AJ52694 Arabidops
AJ611004 Arabidops
AJ611004 Arabidops
AL031004 Arabidops
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AC18491 Rattus no
IG6494 Sequence 14
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AC113213 Rattus no
AR415176 Sequence
AX972010 Sequence
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Makaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Eassicales, Brassicaceae, Arabidopsis.
                                              Arabidops
Arabidops
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           Medicago
Lotus cor
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AC148404 N
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BT008541 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 1027; DB 6; Best Local Similarity 100.0%; Pred. No. 2.3e-287; Matches 1027; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
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Methods and means for modification of
characteristics
Patent: WO 0121822-A 10 29-MAR-2001;
Plant Bioscience Limited (GB)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
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Sequence 10 from Patent W00121822.
AX101036
AX101036.1 GI:13619892
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ATH526944
ATH441294
ATF28M20
ATCHRIV75
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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gene="VNN1"
nlele="Ler"
note="Contains two VP1/ABI3-like B3 domains"
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Levy,Y.Y., Gendall,A.R. and Dean,C.
VRN1, a gene required for response to vernalization
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/protein_id="AAM76973.1"
/db_xref="G1:21734796"
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Levy, Y.Y. and Dean, C.
Direct Submission
Submitted (23-UJL-2000) Molecular
Colney Lane, Norwich, Norfolk NR4
Location/Qualifiers
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/mol_type="mRNA"
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                                             CAAACCTTGTTCACTGGACCAGTTAAAGCTGAAGAGCCCAACGCCAACCCCAAAAATACCT
                                                                                    AAAAAGAGGAGGAAGAAGAAAAATGCTGATCCTGAGGAAATAAACTCATCAGCTCCG
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Methods and means for modification of plant flowering characteristics
characteristics
Patent: Wo 0121822-A 13 29-MAR-2001;
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/organism="synthetic construct"
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/noCe="vrn1-2 mutation"
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CTTGCGGAGAAACAATGGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTCAGT
                            CAAGGATGGTACGAATTCACTCTAGAGAACAACTTAGGAGAAGGAGACGTCTGTGTTTT
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Patent: WO 0121822-A 12 29-WAR-2001;
Plant Bioscience Limited (GB)
Location/Qualifiers
1. 1495
/organism="synthetic construct"
//mol_type="unassigned DNA"
/db xref="taxon:32630"
/note="vrn1-1 mutation"
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Jarity 99.9%; Pred. No. 6.7e-287;
Conservative 0; Mismatchem 1.
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Sequence 12 from Patent
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AX101038.1 GI:13619894
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/db_xref="G1:21734794" /translation="MPRPFFHG.IFSSTIGERGLRVPDKFVSKFKDELSVAVALTVPD GHVMRYGLRKADDKINFRYGLEDEDAEVIPPSESVYERLESSYZIFNLSHSEI NYHSTGLMOSAHNHFKRARLFEDLEDEDAEVIPPSSYVESPLESSTVERNKGYKSASAI QTLFTGPVKAEEPTFPKIPKRGRKKKAADPEEINSSAPRDDDENRSKFYESAAR KRYTAEBERBAINAAFTEEPTNPFFRVVLRPSSYLYRGCIWYLPSGFABKYLSGISGF IKVQLAEKQWPVRCLYKAGRAKFSQGWYEFTLENNLGEGDVCVFELLRTRDFVLKVTA PRVNEXV"  Query Match 63.6%; Score 653.4; DB 8; Length 5000; Best Local Similarity 77.2%; Pred. No. 1.5e-178; Matches 969; Conservative 0; Mismatches 1; Indels 285; Gaps 3; QY SR CTGAGGGTCCCAGATAGTTTGTCGATAGTAGAGATGAGTTGCTGTTGCA 117	3117 CAGAGGCTCCCAGATAAGTTTGTGAAATTCAAGGATGAGGCTTTCGGTTGCTGTTGCA 317  118 CTCACAGTACCTGATGGTCATTTGGCGTGTAAGGAAAGCTGACAAAAATT 177  119 CTCACAGTACCTGATGGTCATGTTTGGCGTGTAGGAAAGCTGACAAAAATT 323  170 CTCACAGTACCTGATGGTCATGTTTGGCGTGTAGGAAAGCTGACAACAAAATT 323  171 TGGTTTCAAGATGGTCATGTTTGTTGACGGTTACTCCATTCGCATTGGTTATCTT 237  172 TGGTTTCAAGATGGTTGGCAAGAGTTTGTTGACGGTTACTCCATTCGCATTGGTTATCTT 237  173 TGGTTTCAAGATGGTTGGCAAGAGTTTGTTGACGTTACTCCATTCGCATTGGTTATCTT 329  238 TTGATTTTAAGATATGAAGAAACTCTGCCTTCAGCGTCACATTTCCAATTTATCCCAC 297	DD 3297 TTGATTTTTAGATGAAACTCTGCCTTCAGCGTCTACATTTTCAATTTATCCCAC 3356  Qy 298 TCTGAGATCAATTACCATTCCACCGGTCTCAGGATTCGCTCACACCACTCAAAGGC 357  DD 3357 TCTGAGATCAATTACCATTCCACCGGTCTCATGGATTCCGCTCACAACCACTTCAAAGGC 3416  Qy 358 GCCCGTTTGTTTGAAGACCTTGAAGATGAGATTCCGCACACACCACTTCTTTGTG 417  DD 3417 GCCGTTTGTTTGAAGACCTTGAAGATGAGAGAGAGAGATTCCTTTCTTT	QY         478 ATCCAAACCTTGTTCACTGGACCAGTTAA         506           Db         3537 ATCCAAACCTTGTTCACTGGACCAGTTAAAGGTGATATTTATAACCAACTGATTCCTTT         3596           QY         507	Qy         562 AAAAATGCTGATCCT         576           Db         3717 AAAATGCTGTTCTGTAAGCACTTTTCCTCTTTGAAATGCTTCAGACTCTTTCAGA         3776           Qy         577	
Qy         760 TACAGAGGTTGCATCATCTATCTTCTGGGTTTGCTCAGAAGTACCTAAGTGGGATC 819           Db         724 TACAGAGGTTGCATCATGTATTTGCCTTCTGGTTTTGCTCAGAAGTACTAAGTGGGATC 783           Qy         820 TCCGGGTTCATCAAGTCCAGCTTGGGAAACAATGGCCTGTTCGATGTCTTACAAA 879           Db         784 TCGGGATTCATCAAGGTCCAGCTAGGGAAACAATGGCCTGTCAGAAGTTCAAA 843           Qy         880 GCCGGAGAGCCAAATTCAGTCAAGGATGGTACCAAATTCACTCTAGAAACAATTAGA 903           Db         844 GCCGGAGAGAGCTAAGTCAAGGTTGGTAAGGTTCACTGTGGAAATAACCTAGGA 903           Qy         940 GAAGGAGAGCTCAGTCAAGGTTGGTAAGGTTCACTGTGGAGAATAACCTAGGA 903           Qy         940 GAAGGACGTCTGTGTTTGAAGTTCATTTGAAAGTGACA 999           Qy         940 GAAGGTCTTGTGTTTGAACTGCTGAGAACCAGAAATTTCGTTTTGAAAGTGACA 999           Qy         940 GAAGGTCTTGTGTCTTTGAACTGCTGAGAAATTTCGTTTTGAAAGTGACG 963	QY         1000 GCCTTTCCAGTCAACGACTACGTCTGA 1026           Db         964 GCCTATCGAGTCAACGACTACGTCTGA 990           RESULT 8         AF289051           LOCUS         DNA         linear         PLN 05-NOV-2003           DEFINITION         Arabidopsis thaliana reduced vernalization response 1 (VRN1) gene, VRN1-Ler allele, complete cds.         ACCESSION         AF289051         G1:21734793	Σ	m . mam . am = " ' '	/mol_type="genomic DNA"  /db_xref="genomic DNA"  /chromosome="3" /map="between mi339 and m560B2" /ecotype="Landsberg erecta" /ecotype="Landsberg erecta" /a1879>4370 /gene="VRN1" /a11ele="Ler" /a11ele="Ler" /a12>4370) /gene="Join(6.1879." 1938,31203567,36643732,38324031,	/glne="vkr" /allele="Ler" join(1879. 1938,31203567,36643732,38324031, 41224370) /gene="vkr" /allele="Ler" /note="contains two VP1/ABI3-like B3 domains" /codon start=1 /product="reduced vernalization response 1" /protein_id="AAM76972.1"

Location/Qualifiers  179186  /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /db_xref="taxon:3702" /chromosome="3" /chromosome="3" /clone="K13813" /clone="K13813" /clone="K13813" /clone="K13813" /clone="K13813" /clone="K13813" /clone="K13813" /clone="K13813" /clone="K13813.1" /clone=id:K13813.1 /clone=id:K13813.1 /clone=id:K13813.1	/ COGNO_BVENTEL / Cevidence=not experimental / protein id="BAB01688.1" / brotein id="BAB01688.1" / brotein id="BAB01688.1" / bxref="GI:19280309" / tanslation="MKTIQEQLPNDLVEEILCRVPATSLRRLRSTCKAWNRLFKGDRI LASKHFEKSAKQFRSLENDYR.FPISFNIHGNSPSLELKSELIDPHSKNSAAPFEI SRVHICKGELLLCSSQLDESRVVWNNPLTGETRWIRTGDFRQKRSFPVGYYYQKDRRS WIKSYKLLCYRGTKYFRTRYPEDSDSWHILDDIIAPRGSIGYSELSVSLKGNTWPAK GVTEERRPTISLLKFDFYTEKSVPVLLPYQSRRLPQASSLSVVREDKLSVLLQLDQSS KTEIWVTNVIDETTKGAVSWTKVLALDLSPHLQIGNDGSFFLGEDKKVVMFCEKLIDE NKKNDMYIVGEDNVVTBVGFGVDEMDGCRAVILNYVPSLVQIERAGGNRKRGH"	Computation (2712.)  Computation (2712.)  Computation product; gb AAF01602.1  gene id: K13B13.2  sinilar to unknown protein"  (codon_start=1  /codon_start=1  /codon_start=1  /protein_id="BB001680.1"  /protein_id="BB001680.1"  /protein_id="BB001680.1"  /protein_id="BB001680.1"  /protein_id="BB001680.1"  /protein_id="RENOTEDEVIRTIPELENERRERRILLISRSSDPPLEFSPPLIA  MVVLAAARIFVYSRLISRRESPLERRERRERNGGRASSASSASTSSDLAS  FRENSESPERRESSAGTVYBEAPHUSCTDEVIRTIPELENERSPROMITSASOUNCL  LEFERGDYWTLPLCTHAFHLECTDEWIRSHPROPLCRTAILGSAGVATTENSPPPLIA  APRIRESLDDESTWINGTHILECTDEWIRSHPROPLCRTAILGSAGVATTENSPPPLIA  APRIRESLDESTRESSESPENTWEBAPTVSPRRYRRESTWINGQSPPGINISRSRINGTSPPPLIA  APRIRESLDESTRESSESPENTWEBAPTVSPRRYRRESTWINGQSPPGINISRSRINGTSPPPLIA  APRIRESLDESTRESSAGVYPYBEAPTVSPRRYRESTWINGQSPPGINISRSRINGTSPPPLIA  APRIRESPPPRRASSAGVYPYBEAPTVSPRRYRESTRESTRESTRY  RSTKSSPFRRRESSAGVYPYBEAPTSFRANGSSSRINGGSPPRASSAGVATA  RSTKSSPFRRRESSAGVYPYBEAPTSFRANGSSSRINGGSPPATA  RSTKSSPFRRRESSAGVYPYBEAPTSFRANGSSSRINGGSPPATA  APRILESPERWRRADTCAARM  complement (join (5713. 5792,5883. 6006,6112. 6349), 6793. 6697,68973. 65913. 1061. 10600. 6112. 6349, 6790. 6697,6897. 65931. 1061. 10600. 6112. 6349, 6790. 6697,6897. 65931. 1061. 10600. 6112. 6349, 6790. 6697,6897. 69931. 1061. 10600. 6112. 6349, 6790. 6697,6897. 69931. 10600. 10600. 6112. 6349, 6790. 6697,6897. 69931. 10600. 10600. 6112. 6349, 6790. 6697,6897. 69931. 10600. 10600. 6112. 6349, 6790. 6697. 6697. 6899. 10600. 10600. 6112. 6349, 67000. earl="distance">61322333377161. 79326,79327771610000. 61320. 6349, 6790. 6697. 6697. 6899. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 6890. 68	YSGSLDKSVKVWRVTESASTVIG" 19263. 19350 /product="tRNA-Tyr" /note="codon recognized: UAC; gene_id:K13E13.5"
FEATURES SOURCE CDS	e E	S C S C S C S C S C S C S C S C S C S C	t RNA
Qy         763 AGAGGTTGCATCAT	4197 CAATGGCCTGTTCGATGTCTTACAAAGCCGGGAGAGCCAAATTCAGTCAG	APONOT35/C APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 APONOT35 A	http://genome.wustl.edu/eddy/tRNAscan-SB/). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between-neighboring submissions. The 5' clone is MCB22 and the 3' clone is MHP21.

widence=not experimental   widence=not experimental   wordence=not experimental   wordence=not experimental   gene id:klisil3.6   gene id:klisil3.6   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   gene id:klisil3.7   wordence=not experimental   gene id:klisil3.7   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordence=not experimental   wordenc	/db_xref="G1:9280317" /translation="MGELDBAFIQAPEHRENTHL/TNSGDFIFSDEIPTIDLSSLEDTH /translation="MGELDBAFIQAPEHRENTHL/TNSGDFIFSDEIPTIDLSSLEDTH HDKTA1AKEIAACKGWGFFQVINHGLPSALRHRYEKTAAEFFNLTTEEKRKVKRRDEV NDWGYHDEEHTKUNYDWRKEIFDFFLODSTIVPASPEREDTELKL/TNGWPQNRPRHE VCQEYAREVEKLAFILELVSISLGLPGDRLTGFFNHYPPPCPNPELALG VGGHYAREVEKLAFILELVSISLGLPGDRLTGFFNHYPPCPNPELALG VGGHYAREVGGALL/VLAQDSRRSDGQWTPVKPISDALIINMGNCIQVWTNDEYW SAEHRVVVNTSKERRSIPFFFFFFFFFFFNHYPPCKKYNWGKFFVSRNR SDFKKLEVENIQDBIFKA"  CODS COMPLEMENT (join (34938. 35198,35304. 35631,36034. 36494))	Query Match   63.6\$; Score 653.4; DB 8; Length 79186; Best Local Similarity   77.2\$; Pred. No. 2.1e-178; Matches 969; Conservative 0; Mismatches 1; Indels 285; Gaps 3; Qy   58 CTGAGGGTCCCAGATAAGTTTGTGAGAAATTCAAGGATGAGTTGCTTGC	3.1		SERVED   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STA	SYPESTYPANK   Qy   SB3 ATAAACTCATCAGCTCCGCGAGATGATCCAGAGAACCGTTCAGAGAGT 642
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TITLE Direct Submission JOURNAL Submitted (12-DEC-2002) Shusei Sato, Kazusa DNA Research Institute, JOURNAL Submitted (12-DEC-2002) Shusei Sato, Kazusa DNA Research Institute, Chiba 192-0918, Japan (B-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337), FAX:81-438-52-3934) FEATURES 1. 78589 1. 78589 1. 78589 1. 78589 1. 78589 1. 78589 1. 78589 1. 78589 1. 78589 1. 78589 1. 78589 1. 78589 1. 78589 1. 796888888888888888888888888888888888888	ORIGIN  Query Match  13.7%; Score 140.4; DB 8; Length 78589; Best Local Similarity 66.6%; Pred. No. 4.4e-29; Matches 201; Conservative 0; Mismatches 101; Indels 0; Gaps 0; Oy 21 TAAGTTGATTTTCCATCCACTATCCAGAAAAACGTCTGAGGGTCCCAGATAAGTTTGT 80		RESULT 15 AC137825/ LOCUS LOCUS LOCUS AC137825 AC137825 AC137825 AC137825 LOCUS Medicago truncatula clone mth2-2311, WORKING DRAFT SEQUENCE, 17 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC13782 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC137825 AC13
00   513 AGAGCCAACGCCAAAATACCTAAAAAGAGAGGAAGAAAAATGCTGA 572	Qy         668         CTGCAGAAGAAGAGAGAGAGCCATCAATGCAGCCAAAACGTTCGAACCAACAACATT         727           Db         28856         CTGCAGAGGAAAGAGAGACCCTCAATGCAGCACAAACCTT         28915           Qy         728         TCTTCAGAGTACTCTCCCGACCATCTATCTACAGAGCTTGCATCATCTATCT	Qy         869 GTCTCTACAAAGCCGGAAGAGCCAAATTCAGTCAAGGATGCTACGATTCACTCTAGAGA 928           Db         29156 GCCTCTACAAGCGAGAGCTAAGTTTAGCCAAGGATGGTTCACACTCGAAGA 29215           Qy         929 ACAACTTAGGAGAGCGTCTGTGTTTCAGCTCACAAACCAAGATTTCGTTT 988           Ill	RESULT 14 AP006145 LOCUS LOCUS DEPINITION LOTUS corniculatus var. japonicus genomic DNA, chromosome 2, clone:Lj703H18, TM0262, complete sequence. ACCESSION AP006145 AP006145 AP006145 LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOTUS LOT

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MYGRRSNYTAVPIPLVGFL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------CATCGAACCCTGAATCTACTGAACCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28232 TGAGCTTTCAGTTGTTTTTGCACTTACAATACCTGATGGTCATGTTT-GCATGTAGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28291 AAGGAAAGCCAACAAAAATCTGGTTTCAAGACGGTTGGCAGGAGTTTGTCAACGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 AAGGAAAGCTGACAACAAAATTTGGTTTCAAGATGGTTGGCAAGAGTTTGTTGACCGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCCATTCGCATTGGTTATCTTTTTGATTATGAAGGAAACTCTGCCTTCAGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28351 CTCCATTCGGATTGGT----TTCAGATACAAAGTTACAGTCTACATTTTCAATTTATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28407 ccacacrereagareaaceace----arreragragreaagererrargeaaredaarre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 CGCTCACAACCACTT---CAAACGCGCCCGTTTGTTTGAAGACCTTGAAGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28463 cécacadaarcagricaacaadaacerecrecarrerrigaadarcereaadaree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 CGAGGICATCITICCTICTICTGTGTACCCATCACCACTICCTGAGICTACAGTACCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          453 CAACAAAGGGTATGCTAGTTCAGCCATCCAAACCTTGTTCACTGGACCAGTTAAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGAGCTTTCGGTTGCTGTTGCACTCACAGTACCTGATGGTCATGTTTGGCGTGTAGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Andreau Division protein; Location of ests 164G18T7 (gi 22764114), 114G10T7 (gi 2597578), and 114G11T7 (gi 2597579)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 125021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Join(28449. .28680,28766. .28965,29065. .29313)
/gene="113F21.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 201; Indels 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="Hypothetical Protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 270.4;
Pred. No. 6.8
                                                                                                                                                              /codon_start=1
/protein_id="AAD43151.1"
/db_xref="G1:5430751"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAD43153.1"
/db_xref="G1:5430753"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Unknown Protein"
                                                                                                                                                                                                                                                                                                                                                                                       /gene="F13F21.7"
23803. .26346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="F13F21.7"
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                                                                                                                                                                                                                                                                                                                                                       23803. .26346
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Best Local Similarity 62.1%;
Matches 694; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28523 TAAGGTCATTTATC
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   join(6527. .6667,6772. .6859,7159. .7311,7597. .7757,
7840. .8514,8612. .8939,9020. .9240,9369. .9546,9658. .10142)
/gene="m13F21.2"
/note="Hypothetical Protein"
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complement(join(15762. .15977,16061. .16492,16809. .16883))
/gene="F13F21.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="wamshiplessposslalrihstyoftlsyskunkdcsposane
akvskrslicralhmesghsgeopkkinfdnilrrtkhvwdnspopvkefpwrrafgn
flolvidialsvvkrifvptlavssisemsycaherklalvppplvigwvyagvloft
alkisprikarvypwhilammfptliklpopyypywgrlivphpangvliralwsmf
fwykktravsgenplonhslete"
1730. .21921
                                                                                                                                                                                                                                                                    / LTAIL ALL OBSENTING THE PERFARKLDROYLLSGDSDGIILMELSTL
CDRTAQILTTLPGHKASVNCTHWLPTSKRAFKKLDROYLLSGDSDGIILMELSTL
NUDKRPYSRSDLSFRANSLASIPREKKVVCDLSGDSDGIILMELSTL
ALALGGLDNKTKLYSRSDLSFRANSLESIPREKKVVCDLSCDFSLPHTTTEIPRSTMLS
ALALGGLDNKTKLYSGDVGSWRREITLASYIEGPVFVSGTFTYQISVESIMLVS
SSQDKVIRIWKLVLVGDVGSWRREITLASYIEGPVFVSGTFTYQISVESVLIGHEDWV
YSVEWOPPVIDPIDGRLVNHOPLSILSASMDKTTMINRPKTTGVWTVVVCVGELSHC
ALGFYGGWWASPNSLSILAHGYGGAFHLWRNVSSSKESENWQMCKVPSGHFAAVTDVTW
ARTGFYLLSVSQDQTTTRVFSAWKNDEGNRADEHWHELARPOYHGHDINCVANVVCKG
NHRFVSGAEEKVVRVFEAPLSFLKTLNHTCAGGEGSFPEDLQADVQVLGANMSALGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon start=1
/product="geranyl geranyl pyrophosphate synthase"
/protein id="AAA94148.1"
/db_xref="Gi:s430748"
/translation="MRPRYSLILSAMRLIRPSNRRLSSIASSDSEFISYMKNKAKSIN
KALDNSIPLCNNFVPLMEPVLEVHKAMRYTLLPGGKRVRPMLCLVACELVGGGESTAM
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KTINNFQMNKALAKHYWALNDGDGCFRUYKEEDVDETSGERDEKDVKTEBALENNEEE
SREEDENSVRKKKKKKKKPKAKGEFRYKKGGGFRYVCSLSPETQAFTGTPQLARTBVV
KMLWKYIKENNLQDPSDKRTIICDESLRSLFPVESINNFQWNKQLAKHIWPLVVGDDEA
GTTNDPEKGKQKMKMETDEVKNIKSSTFLNYIDNDESNEEKÄTSSRIKTEE"
complement [15762. .16883)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHGNELFSLCSDHKGNLVASSCKAQSASMAEIMLMEVGTWKAVGRLQSHSLTVTHLEF
SYDDTLLLSVSRDRHFSVFSIQRTDNGEVSHKLMAKVBAHKRIIWACSMNPFGHQFAT
SSRDKTVKIWSVENDARIKQILVLPPFGSSVTAVAWTGLDRNEKSGCVAVGMESGLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAACAVEMIHAASLILDDLPCMDDDSLRRGKPTNHKVFGEKTSILASNALRSLAVKQT
LASTSLGVTSERVLRAVQEMARAVGTEGLVAGQAADLAGERMSFKNEDDELRYLELMH
VHKTAVLVEAAAVVGAIMGGGSDEEIERLKSYARCVGLMFQVMDDVLDETKSSEELGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LISNVKI I ETEEGTTATAALALRLEPFMCHVSAVNRLAWRPTEKCESNQSLRWLTSCGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAGKDLITGKLITYPKVMGVDNAREYAKRLINREAQEHLQGFDSDKVVPLLSLADYIVKR
Qn"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFVREQIDAFLESDALLESKPEQEEEDCNGDQNDEEGSENDDDKTELPVKAKKRGGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKPIYLHSSSEPLERNGGGEGLDTFETVPEAAPAELKEPPIEDQLAFHTLWPESHKLY
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12784. .12898,12987. .13143,13236. .13410,13500. .13602,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F13F21.3"
/note="97% identical to geranyl geranyl pyrophosphate
synthase [Arabidopsis thaliana] gi|2578822."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ests VBVQD12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="F13F21.4"
/note="Hypothetical Protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="F13F21.3"
complement(10370. .11380)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (12218. .14173)
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|protein_id="AAD43149.1"
|db_xref="GI:5430749"
                                                                                                                                                              /codon_start=1
/protein_id="AAD43147.1"
/db_xref="GI:5430747"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (10370. .11380)
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/db_xref="G1:5430750"
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21730. .21921
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
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                                                                                                     GATTCCGCACAGAATCAGTTCAACAAACGTGCTCGATTGTTTGAAGATCCTGAACTCAAA
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Stress-regulated genes of plants, transgenic plants containing same, and methods of use
Patent: WO 0216655-A 273 28-FEB-2002;
The Scripps Research Institute (US); Syngenta Participations A (CH)
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    . 681
    /organism="Arabidopsis thaliana"

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PIKLOUGEKQMPVRCLYKAGRAKFSQGWYEFTLENNIGEGDVCVFELLRTRDFVLEVT
APRVNEYV"
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      Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 1146)
I (bases I to 1146)
Chen, M., Chen, M., Chen, M., Chen, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 GGACTAAGGAAAGCTGACAACAAAATTTGGTTTCAAGATGGTTGGCAAGAGTTTGTTGAC 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen, M. Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN arbidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                   Nayen, M., Karlin-Neumann, G., Southwick, A., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Direct Submission
Submitted (25-JUN-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                       e-mail for correspondence: arab@sequence.stanford.edu
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Pred. No. 2.8e-117;
0; Mismatches 194;
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/chromosome="I"
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177. .857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pederspiel, N.A., Falm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, B., Dunn, P., Gonzalez, A., Kremenetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission
Submitted (09-UIL-1999) DNA Sequencing and Technology Center, granford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                          Chases 1 to 125021)

Pederspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buchler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission
                                                                                                                                                                                                                                                                         Submitted (06-MAY-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304
Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriuni, M., Vysotskaia, V.S., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Unpublished
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1 (bases 1 to 125021)
Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P.,
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                                                                                                                          Length 681;
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                                                                                                                       Score 397.6; DB 6;
Pred. No. 3.2e-104;
0; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                      67 AAAGATGCTAAGGTCATTTATCCATCGAAC-----
                            DNA"
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Arabidopsis thaliana
                          /mol_type="unassigned
/db_xref="taxon:3702"
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AC007504.3 GI:5430745
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Best Local Similarity 76.6%;
Matches 538; Conservative
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VERSION
KEYWORDS
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on Jul 9, 1999 this sequence version replaced gi:5019265.

e-mail for correspondence: arabasequence.stanford.edu
Genes with similarity to proteins in the databases are described
as 'putative', 'like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge,
http://gromic.stanford.edu.chris/GENSCANW html), Fexa (V.Solovyev
& A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/),
NetPlantGene (S. M. Hebesgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/NetPlantGene.html) and
eMocif(Nevill-Manning, C.G. Wu, T.D. & Brutlag, D.L.,
http://motif.stanford.edu/projects.html):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein id="AAD43146.1"
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/db xref="G1:5430746"
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KAYKRPSSTTSSSOVETLEEDIPAGYSGFYAFVSOKYGSSGKSELDIYLGEPFLDMA
AFRHFWYLAYWGDNSCRFKELSSMACDVLSIPITTVASESSFSIGSGVLSKYRSSLLP
ENIQALICTRNWLRGFPKEGEBEEEVEBEKEBEKEERA"
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/mol_type="genomic DNA"
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/gene="F13F21.1"
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/gene="F13F21.2"
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AUTHORS

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155226 AAGTAATGAAGCGTCTCTTTGGAAAACGTCTTACTATTTTCGAAGAAATGGAAGATGA 155167
      155466 TGGTGGTGATATTTCTCCAACTGTTACTCTCACAGTTCCTGATGGCAGTGTGTGGCGTGT 155407
                                                                                                                                                                                                                                330 GGATTCCGCTCACAACCACTT---CAAACGCGCCCGTTTGTTTGAAGACCTTGAAGATGA 386
                                                                   155346 AAACTATTCCATTAGTACTGGATACTTGTTGGTATTCAAATATGAAGGAAAGTCGCATTT
                                                                                                                                                                  270 CAGCGTCTACATTTTCAATTTATCCCACTCTGAGATCAATTACCATTCCACCGGTCTCAT
                                                                                                  210 CCGTTACTCCATTCGCATTGGTTATCTTTTGATTTTTAGATATGAAGGAAACTCTGCCTT
                                    150 AGGACTAAGGAAAAGCTGACAACAAAATTTGGTTTCAAGATGGTTGGCAAGAGTTTGTTGA
                                                                                                                                                                                                                                                                                                                            155166 AGATTCTGTTGAAATCATGGAATCGTC 155140
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3 (bases 1 to 243777)
Shaull, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B.,
Cook, D., Kim, D. and Roe, B.A.
Direct Submission
Submitted (13-AUG-2004) Department Of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 CAAGGATGAGCTTTCGGTTGCTGTTGCACTCACAGTACCTGATGGTCATGTTTGGCGTGT 149
                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                               OK 73019, USA
On Aug 3, 2004 this sequence version replaced gi:50540779
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/mol_type="genomic DNA"
/clone="mth2-23j1"
/clone_lib="Medicago truncatula BAC library H2"
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JOURNAL
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Aak51957 Human pol Adm03188 Human cDN Aba98590 Human tes Adb80383 Human MDD

Rice gene Tumour su Gene enco

Aav74539 Staphyloc Ach2164 Human adu Aax40160 Gastric c Aas46671 Tumour su Adc03457 Wheat flo Acx46225 Human dit Aax52941 Human pol Abl20142 Drosophil

Aas41706 Genomic a Aba66788 Human gen Abv84125 Human gen Abs41104 Genomic a Aba66786 Human gen Abv84123 Human pol Acf72703 Staphyloc Aca20939 Prokaryot Ada37119 DNA encod Aby4539 Staphyloc Ach21644 Human adu

OM nucleic

Run on:

Sequence:

Searched:

Database

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Result Š.

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Novel VRN1 polynucleotide sequence encoding a polypeptide which alters vernalization response of plant in which VRN1 nucleic acid is expressed, useful for influencing and assessing vernalization phenotype of plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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                                                                                                           ADM03188
ABA98590
ADB80383
                                                                                                                                                                                         AAS41706
ABA06788
ABV84125
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ABA06786
ABV84123
AC72703
ACA20939
ADA32719
AAV74539
ACH21644
AAX40160
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269. .1294
/*tag= a
/product= "VRN1"
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production of crop plants, where they are able to control the timing of flowering, the duration of vernalisation required, the optimum temperature, or even eliminate the need for vernalisation completely. The
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                                                                                                                                               ACAGTACCTGATGGTCATGTTTGGCGTGTAGGACTAAGGAAAAGCTGACAAAATTTTGG
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                                                               Length 1495;
                                            G; 458 T; 0 U; 0 Other;
                                                                                  Indels
                                                               ; Score 1027; DB 4;
; Pred. No. 6.1e-312;
0; Mismatches 0;
                           present sequence is the VRN1 coding sequence
                                              Sequence 1495 BP; 403 A; 322 C; 312
                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1027; Conservative 0;
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This invention relates to a novel method for altering one or more plant contracteristics. Specifically, it refers to identifying genes that are up characteristics. Specifically, it refers to identifying genes that are up or down-regulated in transgenic plants overexpressing the heterodimeric content for the properties and using these sequences to alter plant characteristics accordingly. The present invention describes consymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture contents of plants and animal feed products. Accordingly, these cach relative to the corresponding wild type plants, Accordingly, these cach relative to the corresponding wild type plants, Accordingly, these cach relative to the useful as positive or negative selectable markers curing transformation of cells or tissues. The identified genes play a curing transformation of cells or tissues the identified genes play a coll in a variety of biological processes such as DNA replication, cell coll in a variety of biological processes such as DNA replication, cell cranscription factors. This polymulcleotide sequence is thate cress cDNA repressed 1.3 fold or more in plants overexpressing the EZFA/DPa
                                                           1169 CAAGGATGGTACGAATTCACTCTAGAGAACAACTTAGGAGAAGGAGGACGTCTGTGTTT 1228
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                                     GAGCTGCTCAGAACCAGAGATTTCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGTAC
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                                                                                                                                                                                                                                                                                                                                                                                            gene; 88; plant; transgenic; B2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabol.
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P-PSDB; ADN73923.
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Mismatches

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Matches 1026; Conservative

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                              Arabidopsis thaliana DNA fragment SEQ ID NO: 25332
                    AAC39629 standard; DNA; 1510 BP.
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99US-0132487P.
99US-0132867P.
99US-0132863P.
99US-0134218P.
99US-0134218P.
99US-013421P.
99US-0134370P.
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23-APR-1999;
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09-MAR-1999;
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25-MAR-1999;
01-APR-1999;
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16-APR-1999;
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                                                                                                                 CTGAGGGTCCCAGATAAGTTTGTGAGTAAATTCAAGGATGAGCTTTCGGTTGCTGTTGCA
                                                                                                                                                                                                                        CTCACAGTACCTGATGGTCATGTTTGGCGTGTAGGACTAAGGAAAGCTGACAAAATT
                                                                                                                                                                                                                                                                                                             TGGTTTCAAGATGGTTGGCAAGAGTTTGTTGACCGTTACTCCCATTCGCATTGGTTATCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTGAGATCAATTACCATTCCACCGGTCTCATGGATTCCGCTCACAACCACTTCAAACGC
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                                                                                         Gaps
                                                                                       Indels 285;
Sequence 5000 BP; 1447 A; 871 C; 931 G; 1750 T; 0 U; 1 Other;
                                           Length 5000;
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Pred. No. 5.7e-194;
1; Mismatches 1;
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Best Local Similarity 77.1%;
Matches 968; Conservative
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 Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                  TTTGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAGTCCAGCTTGCGGAGAAA
                                                                                                              Arabidopsis thaliana DNA fragment SEQ ID NO: 19075.
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                                                                                                                                                                        AAC37903 standard; DNA; 753 BP
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        21-AUG-1999 j
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TITGAGCTGCTCAGAACCAGAGATTTCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAG 1017
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                                                                                                                                                                         1 AACCAAACCTTGTTCACTGGACCAGTTAAAGCTGAAGAGCCAACGCCAACGCCAAAATA
                                                                                                                                           61 CCTAAAAAAGAGAGGAAGGAAGAAGAAAAAATGCTGATCCTGAGGAAATAAACTCATCAGCT
                                                                                                                                                                                                                         AGAACCGTGACTGCAGAAGAAGAGAGAGAGCCATCAATGCAGCCAAAACGTTCGAACCA
                                                                                                                                                                                                                                                                      538 CCTAAAAAGAGAGGAAGAAGAAAAATGCTGATCCTGAGGAAATAAACTCATCAGCT
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                                                                               478 ATCCAAACCTTGTTCACTGGACCAGTTAAAGCTGAAGAGCCAACGCCAACCCCAAAAATA
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                                   753;
                                   Length
                                                         Indels
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                                 Query Match 53.4%; Score 548.4; DB 3; Best Local Similarity 99.8%; Pred. No. 1.7e-161; Matches 549; Conservative 0; Mismatches 1;
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99US-0123180P.
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| TACGTCTGAA 550
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                               Query Match
Best Local Similarity
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05-MAR-1999;
09-MAR-1999;
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PR 22-WR-1999 90US-012278PP.
PR 12-WR-1999 90US-012378PP.
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                                                                                                                CCATCATATCTATACAGAGGTTGCATCATGTACTTGCCATCTGGGTTTGCTGAGAAATAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGAAAGTGACACCTTTCGAGTCAACGAGTACGTCTGA 1026
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29-MAR-1999;
01-APR-1999;
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08-APR-1999;
16-APR-1999;
19-APR-1999;
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23-APR-1999;
23-APR-1999;
28-APR-1999;
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30-APR-1999;
04-MAY-1999;
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Best Local Similarity 73.5%;
Matches 646; Conservative
07-0CT-1999

08-0CT-1999

13-0CT-1999

13-0CT-1999

14-0CT-1999

14-0CT-1999

14-0CT-1999

14-0CT-1999

14-0CT-1999

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RR 22-WK-1999) 9908-0115124P
RR 22-WK-1999) 9908-0115152P
RR 22-WK-1999) 9908-0115152P
RR 22-WK-1999) 9908-0115152P
RR 01-UW-1999) 9908-0115152P
RR 01-UW-1999) 9908-0115122P
RR 10-UW-1999) 9908-011722P
RR 11-UW-1999) 9908-011
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9905-0145951P9905-0146386P9905-0147038P9905-0147038P9905-0147038P9905-0147103P9905-0147103P9905-0147103P9905-0147103P9905-0147103P9905-0147103P9905-0147103P9905-0147103P9905-0147103P9905-0147103P9905-0147103P9905-014972P9905-014972P9905-014972P9905-014972P9905-014972P9905-014972P9905-014972P9905-014972P9905-015908P9905-015908P9905-015908P9905-015908P9905-015908P9905-015908P9905-015908P9905-015908P9905-015908P9905-015908P9905-015908P9905-015908P9905-015908P9905-015908P9905-015908P9905-015908P9905-015908P9905-015908P9905-015908P9905-015908P9905-016908P9905-016908P9905-016908P9905-016908P-

24-SEP-1999, 28-SEP-1999, 29-SEP-1999,

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AAC37617 standard; DNA; 1344 BP.
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25-MAR-1999;
29-MAR-1999;
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11-MAY-1999;
14-MAY-1999;
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14-MAY-1999;
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23-APR-1999
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20-MAY-1999;
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                                                                                                                        Gaps
                                                                                                                     38;
                                                                                                Length 1396;
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                                                                                              Score 441; DB 3; L, Pred. No. 1.5e-127; 0; Mismatches 195;
 99US-0161359P.
99US-016136DP.
99US-016132DP.
99US-016192DP.
99US-0161932P.
99US-0162142P.
                                                                                                                                                                                                                                                                                                                                                               GATGCTAAGGTCATTTATC
                                                                                               42.9%;
                                                                                                                       Conservative
                                                                                              Ouery Match
Best Local Similarity
Matches 646; Conserv
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway; metabolic pathway;
promoter; termination sequence; ss.
                                       Arabidopsis thaliana DNA fragment SEQ ID NO: 18041.
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99US-0123180F.
99US-0123548F.
99US-0125788F.
99US-0126264F.
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99US-0130077P.
99US-0130449P.
99US-0130510P.
99US-0130891P.
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99US-0132485P.
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99US-0135353P.
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                                                                                 Arabidopsis thaliana
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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynuclectides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynuclectides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                               Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAACCGTGACTGCAGAAGAAAAAGAGA 684
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                                                                                                                                           Claim 144; SEQ ID NO 273; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                              Score 397.6; DB 6; Length 66 Pred. No. 4.6e-114; 0; Mismatches 134; Indels
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  (SCRI ) SCRIPPS RES INST.
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                                            Wang X,
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Best Local Similarity 76.6%;
Matches 538; Conservative (
                                            Kreps J,
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                                           Harper JF,
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GATTCCGCTCACAACCACTT---CAAACGCGCCCGTTTGTTTGAAGACCTTGAAGAAAA
                                                                               GATGCTAAGGTCATTTATC-------CATGGAACCCTGAATTTACTGAA
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                                                                                                            CCAGCCAACAAAGGGTATGCTAGTTCAGCCATCCAAACCTTGTTCACTGGACCAGTTAAA
                                                                                                                                                                  GCTGAAGAGCCAACGCCAACACAAAATACCTAAAAAGAGAGGAGGAAGAAGAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel Arabidopsis thaliana nucleic acid useful for identifying homologous or related genes, and to create genetically modified and transgenic organisms, such as plant cells and plants.
                                                                                                                                                                                                                                                                                                                                                                     Transgenic plant; plant; genetically modified cell; environmental stress; ribozyme creation; disease resistance; stress tolerance; fungicide screening; insecticide screening; gene; ds.
  580 GAGAACAATATAGGCGAAGGAGATGTATGTGTGTTTGAGCTACTCAGAACTCGGGATTTC 639
                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana expressed sequence related polynucleotide #237.
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JP, Haas V
Hoffman N;
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Ledford BL, Woessner
, Davis KR, Allen K,
                                                                        Claim 1; SEQ ID NO 237; 43pp; English.
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A, Mathew AV, I
er M, Slater T,
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ARK62122 Standard; DNA; 426 BP. XX

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manipulation of certains the entrains that are capable of withstanding a particular disease or environmental stress, for enhancing or inhibiting production of biosynthetic product in a plant, for producing production of biosynthetic product in a plant, for producing polypeptides, as probes for the detection of mRNA in biological samples, to generate additional copies of (1), to generate ribozymes or oligonucleotides, as single stranded DNA probes or as triple-strand transgenic organisms, such as plant cells and plants. (II) or (III) is useful for introducing or improving disease resistance and stress useful for introducing or improving disease resistance, and stress to clerance in plants, screening biological active agents, e.g., fungicides, insecticides, etc., and for elucidating biochemical pathways. (III) is useful as crops for their enhanced diseased resistance, enhanced convironmental stress, or to produce a factor. This sequence represents a nucleic acid that may correspond to naturally corrunting Arabidopsis thaliana expressed sequences. Note: The sequence contains the patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at
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Pred. No. 5.2e-82;
0; Mismatches 3; Indels 0;
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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23-APR-1999;
23-APR-1999;
28-APR-1999;
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  1843 AAGGAAAGCCAACAACAAATCTGGTTTCAAGACGGTTGGCAGAGATTTGTCAACCGTTT 1902
                                                                                                                         The invention relates to identifying a stress condition to which a plant representative of expressed polymucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polymucleotides in the plant cell with an detecting a profile of expressed polymucleotides in the plant cell genome; and (b) detecting a profile of expressed polymucleotides in the plant cell production of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abloric stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                             1784 réadcitricadrierritrice de recentada récida récident de la 1842
                                                                    Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                                                                                                      Claim 144; SEQ ID NO 2973; 577pp + Sequence Listing; English.
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Pred. No. 1.8e-20;
0; Mismatches 15; Indels
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Pred. No. 8.5e-10;
0; Mismatches 146; Indels
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                            990S-01593299-990S-01593309-990S-01593310-990S-01596378-990S-01596389-990S-01607419-990S-0160708-990S-0160989-990S-0161908-990S-01613619-990S-01613619-990S-01613619-990S-01613619-990S-01613619-990S-0161928-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01619329-990S-01621422-
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Matches 154; Conservative
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Garcia CA, Kricker M, Slater T,
Hurban P;
    27-JAN-2000; 2000US-0178512P.
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                                                  WOESSNER J P
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                                  RAMBAKA J G.
                                          MATHEW A V.
LEDFORD B L.
                       PRICE J L.
RAINES T M.
           GORLACH J.
                                                                     DAVIS K R.
ALLEN K.
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HURBAN P.
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                                                             KRICKER M.
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                                                         GARC/
                   HAMI/
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Hamilton CM,

Price JL, Raines TM, Yu Y; Ledford BL, Woessner JP, Haas WD; Davis KR, Allen K, Hoffman N;

Novel Arabidopsis thaliana nucleic acid useful for identifying homologous or related genes, and to create genetically modified and transgenic organisms, such as plant cells and plants. Claim 1; SEQ ID NO 569; 43pp; English.

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The invention describes an Arabidopsis thaliana nucleic acid (I). The polypeptide (II) encoded by (I), transgenic plant (III) or genetically conditioned cell (IV) are useful for screening a candidate agent for its biological effect, by combining the candidate agent with (II), (III) or (IV), and determining the expension or related genes, for convocations that modulate the candidate agent on (II), (III) or (IV). (I) is useful for identifying homologous or related genes, for producing compositions that modulate the expression or function of its encoded protein, for mapping innoctional regions of the protein, in diagnosis, for studying associated physiological pathways, for genetic manipulation of cells, preferably plant cells, in screening assays of various plant strains to determine the strains that are capable of various production of blosynthetic product in a plant, for cor inhibiting production of blosynthetic product in a plant, for cor inhibiting production of blosynthetic product in a plant, for correct additional copies of (I), to generate ribozymes or colligonoucleotides, as probes for the detection of maNA in biological samples, to generate additional copies of (I), to generate ribozymes or colligonoucleotides, as probes for the detection of maNA in biological confined organisms, such as plant cells and plants. (II) or (III) is constined for introducing or improving disease resistance and stress consting behavase. Constined in plants, screening biological active agents, e.g., fungicides, insecticides, etc., and for elucidating biochemical pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       traits of interest, for screening programs, as crops which exhibit enhanced tolerance to environmental stress, or to produce a factor. This sequence represents a nucleic acid that may correspond to naturally occurring Arabidopsis thaliana expressed sequences. Note: The sequence data for this patent did not form part of the printed specification, but sequence obtained in electronic format directly from the US patent office at sequence.uspto.gov/sequence.thml?DocID=999909770423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 411 BP; 155 A; 92 C; 57 G; 107 T; 0 U; 0 Other;
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411 GAAGGAGATGTATATGTGTTTGAGCTACTCGGGATTTTGGTTCTCGAAGTCACC 352
                                                                                                                                                                 Search completed: December 30, 2004, 13:26:53 Job time : 605 secs
                                                                                                        351 GCCTTTCGTGTCAATGAGTATGTGTGA 325
                                                                 1000 GCCTTTCGAGTCAACGAGTACGTCTGA
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6.1%; Score 63; DB 8; Length 411; 12.8%; Pred. No. 7e-09; ve 0; Mismatches 15; Indels

82.88;

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0; Gaps

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OM nucleic

Run on:

Sequence:

Searched:

Sequence 5, Sequence 1, Sequence 1,

Sequence Sequence Sequence

Sequence Sequence

Sequence

Sequence Sequence S

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4.2%; Score 43.2; DB 1; Length 7218;
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APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGE, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: ALexandria
STREET: UA
COUNTRY: USA
CONTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: USA
STEMM: PC compatible
COMPUTER: USA
COMPUTER: USA
STEMM: PARENTING SYSTEM: RC COMPUTER: USA
COMPUTER: USA
COMPUTER: USA
COMPUTER: USA
STEMM: DEPLICATION NUMBER: US/08/232,463
US-08-430-024-1

US-08-702-1

US-08-923-992A-5

US-08-923-992A-5

US-08-923-992A-5

US-08-923-992A-1

US-08-923-992A-1

US-08-923-992A-1

US-08-923-992A-1

US-08-923-992A-1

US-08-923-992A-1

US-08-923-992A-1

US-09-925-041-5

US-09-411-812A-4

US-09-411-812A-4

US-09-411-812A-4

US-09-590-113-4

US-09-590-113-4

US-09-683-62B-74

US-09-683-62B-74

US-09-683-62B-74

US-09-683-62B-74

US-09-683-62B-74
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APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATORNAY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTER.STICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLGY: linear
IMMEDIATE SOURCE:
                                                                    2617
3294
3284
4200
4200
4200
90050
90050
485
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485
1141
2922
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US-08-232-463-14
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US-08-232-463-14/c
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Sequence 22, Appl
Sequence 14, Appl
                                                                                                                                                                                                         December 30, 2004, 12:43:00 ; Search time 113 Seconds (without alignments) 6460.002 Million cell updates/sec
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-620-312D-977
US-08-961-527-168
US-09-221-017B-1090
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US-09-328-352-4006
US-08-956-171E-228
US-08-781-986A-228
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US-09-270-767-29582
US-09-270-767-13580
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US-09-107-532A-1348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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US-09-692-570-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-270-767-358
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1027
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                     nucleic search, using sw model
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Maximum DB seq length: 200000000
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Match Length
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Result No.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         388 GAIGCCGAGGICAICTITCCTITCTGIGIACCCAICACCACTICCTGAGICTACAGIA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448 CCAGCCAACAAAGGGTATGCTAGTTCAGCCATCCAAACCTTGTTCACTGGACCAGTTAAA 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       543 AAAGAGAGGAAGGAAGAAAAAAATGCTGATCCTGAGGAAATAAACTCATCAGCTCCGCG 602
                                                                                                                                                             603 AGATGATGATCCAGAGAACCGTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAGAAC 662
                                                                                                                                                                                                                 663 CGTGACTGCAGAAGAAGAGAGAGAGCCATCAATGCAGCCAAAAACGTTCGAACCAACAAA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 MSTRWYCYMCWKCCMYRGRRCAWYTMARGRMWSYAWGKWKSMRSAMSMCTRMYYKKGSTY 244
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                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRYWRWAMAMWEMWATMAMMYYWYWRAMKRRWWWRKWRSWSWMWMAWGMTRW 11
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Pred. No. 0.0066;
                                                                                                                                                                                                                                                                                                       Sequence 2813.7 Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Goldano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
TITLE OF ILING DATE: 009/621,976
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
                         6; Conservative 148; Mismatches
           2.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , NAME/KEY: CDS
; LOCATION: 235.399
US-09-621-976-2813
                                                                                                                                                                                                                                                                                     RESULT 2
US-09-621-976-2813/c
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                            Matches
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RESULT 3

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NAME/KEY: promoter
1. LOCATION: (1)..(1141)
2. COCATION: (1)..(1141)
3. OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAEI promoters
US-09-806-7088-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 DDDTKYHMMNNGCBTVTWAVRYKTDRDWSBKRANYGMBWWKNWSYDVTYYWWVWDDMCK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGATCCAGAGAACCGTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAGAAACGTG 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              722 ACCCTTTCTTCAGAGTGGTTCTGCGACCATCCTATCTATACAGAGGTTGCATCATGTATC 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 KADMDWBGTYNNNNNGGRTYYGWTKNKKAWYYYKWKANNCKWRAWDHKTCTHNNTTWWKM 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGCGGAGAAACAATGGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTCAGTC 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGATGGTACGAATTCACTCTAGAGAACAACTTAGGAGAAGGAGACGTCTGTGTTTG 961
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Sequence 22, Application US/09806708B

Sequence 22, Application US/09806708B

Patent No. 6784342

GENERAL INFORMATION:
PAPLICANT: The University of British Columbia

TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants

TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants

CURRENT APPLICATION NUMBER: US/09/806,708B

CURRENT PLING DATE: 1999-08-04

PRIOR PILING DATE: 1999-08-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.0

SEQ ID NO 22

LENGTH: 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  547 AGAGGGAGGAAGAAAAAAATGCTGATCCTGAGGAAATAAACTCATCAGCTCCGCGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       667 ACTGCAGAAGAAAGA-----GAGAGAGCCATCAATGCAGCCAAAAACGTTCGAACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DRINER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-08-232-463-14
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Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                                                                                                                                                                                                                                                                                                                                                                                                     2342 ATGAGGTTATAGATATCTACACCTGCCTCACCTGCAACCATTTCATCTTCGTTTACACGA 2283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2282 ATAACGATACGAGAAGCATCTACATATTCAATTACACCGCCACGGTTTGCGATTACACAC 2223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 GARACTCTGCCTTCAGCGTCTACATTTTCCATTTATCCCACTCTGAGATCAATTACCATT 316
                                                                                                                                                                                                                                                                                                        Gape
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                                                                                                                                                                                                                                                  Query Match 3.5%; Score 35.8; DB 4; Length 4143; Best Local Similarity 52.3%; Pred. No. 1.1; Matches 79; Conservative 0; Mismatches 72; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2222 ACACCAGAGTCACGTGCAACGTTCGCTTCCA 2192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 CCACCGGTCTCATGGATTCCGCTCACAACCA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
                         CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 228, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 4488 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                            j ORGANISM: Acinetobacter baumannii
US-09-328-352-4006
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INFORMATION FOR SEQ ID NO: 228:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
       FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-08-956-171E-228
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US-09-328-352-4006/c
US-09-328-352-4006/c
; Sequence 4006, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
APPLICANT: GENY L. Breton et al.
; TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 TTTGTTGACCGTTACTCCATTCGCATTGGTTATCTTTTGATTTTAGATATGAAGGAAAC 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 GATGAAGATGCCGAGGTCATCTTTCCTTCTTGTGTACCCCATCACCACTTCCTGAGTCT 441
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                                                                                                                                                                ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTATION NUMBER: 29,768
REGISTATION NUMBER: 29,768
REGISTATION NUMBER: 29,768
REGISTATION NUMBER: 30472/114 IMMU
TELECOMMUNICATION:
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS: FOLGY & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
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STRANDEDNESS: single
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                                                                                                  CITY: Alexandria
STATE: VA
                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-232-463-14
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                                                                                                                                                                                                                                  Sequence 228, Application US/08781986A
Sequence 229, Application US/08781986A
Sequence 2373248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           554 GGAAGAAGAAAATGCTGATCCTGAGGAAATAAACTCATCAGCTCCGCGAGATGATGAT
                                                                                                                                                                                             494 CIGGACCAGTIAAAGCIGAAGAGCCAACGCCAACCCCAAAAAIACCTAAAAAGAAGAGGGA 553
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                                                                                                                                                                                                                                                                                                           494 CTGGACCAGTTAAAGCTGAAGACCAACGCCAACCCCAAAAATACCTAAAAAGAGAGGGA
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                                                                                                    Query Match
3.5%; Score 35.8; DB 4; Length 4488;
Best Local Similarity 56.3%; Pred. No. 1.1;
Matches 67; Conservative 0; Mismatches 52; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
;
SEQUENCE DESCRIPTION: SEQ ID NO: 228:
US-08-956-171E-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLLING DATE:
APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BERSON, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248
TELECOMMUNICATION INFORMATION:
TELEPONE: (301) 309-8512
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 228:
SEQUENCE GHARACTERISTICS:
SEQUENCE: GHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4488 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 56.3
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-781-986A-228
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US-08-781-986A-228
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RESULT

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US-09-621-976-2813

'Sequence 2813, Application US/09621976
'Patent No. 6639063
'GENERAL INFORMATION:
'APPLICANT: Unmas Milne Edwards, J.B.
APPLICANT: JODERT, S.
'APPLICANT: Glordano, J.Y.
'TITLE OF INVENTION: ESTS and Encoded Human Proteins.'
'TITLE OF INVENTION: ESTS and Encoded Human Proteins.'
'CURRENT APPLICATION NUMBER: US/09/621,976
'CURRENT FILING DATE: 2000-07-21
'NUMBER OF SEQ ID NOS: 19335
'SOFTWARE: Patent.pm
'SEQ ID NO 2813
'LENGTH: 832
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,164
FILING DATE: July 17, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 621851man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5499 - JEL/NDH/SLH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATCTTCCTTCTGGGTTTGCTGAGAAGTACCTAAGTGGGA 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35.2; DE
Pred. No. 1.5;
0; Mismatches
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 341 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.4
Best Local Similarity 51.2
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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LOCATION: (234187). (234187)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (234220). (234220)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (234814)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
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ER INFORMATION: n equals a, t

E/KEY: misc.feature.

ATION: (559167)..(559167)

ER INFORMATION: n equals a, t
                    OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (98159). (98159). OTHER INFORMATION: n equals a,
                                                                                                                                       NAME/KEY: misc feature
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a,
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OCATION: (163385)..(163385)
THER INFORMATION: n equals a,
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LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a,
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LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a,
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LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a,
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LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a,
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LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a,
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COCATION: (312593)..(312993)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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FION: (559241)..(559241)
RINFORMATION: n equals a,
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LOCATION: (657081) ..(657081)
OTHER INFORMATION: n equals a,
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ION: (622708)..(622708)
INFORMATION: n equals a,
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FION: (312837)..(312837)
R INFORMATION: n equals a,
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                                                                                    NAME/KEY: misc feature
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals
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LOCATION: (148948) .. (148948)
OTHER INFORMATION: n equals
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COCATION: (98343)..(98343)
OTHER INFORMATION: n equals
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COCATION: (231980)..(231980)
OTHER INFORMATION: n equals
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LOCATION: (657203)..(657203)
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LOCATION: (600992)..(600992)
     (98120)..(98120)
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Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION:
TITLE OF INVENTION:
Patent No. 6503729
TITLE OF INVENTION:
PATENT NO. 6503729
TITLE OF INVENTION:
PATENT NO. 6503729
TITLE OF INVENTION:
PATENT NO. 6503729
TITLE OF INVENTION:
FILE REFERENCE: 1997-08-22
CURRENT FILING DATE: 1997-08-22
REIOR PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                              391 GCCGAGGTCATCTTTCTTTCTGTGTACCCATCACCACTTCCTGAGTCTACAGTACCA 450
                                                                                                                                                                                                                                                                                                                                    451 GCCAACAAAGGGTATGCTAGTTCAGCCATCCAAACCTTGTTCACTGGACCAGTTAAAGCT 510
                                                                                                                                                                                                                                                                                                                                                           257 SKTSYKSMMCWIRSWKYCYIKARWIGYYCYRKGGMWGKRGRWYASKKYMWKRWWWGWAR 316
                                                                                                                                                                                                                                                                                  571 GATCCTGAGGAAATAAACTCATCAGCTCCGCGAGATGATGATCCAGAGAACCGTTCAAAG 630
                                                                                                                                                                                                                  18 KWKWSWSYWMYWKWYYMKTYWRWRRKKKKAWWKYWKTWTWWYWRYAMWGTYKKKAMCRTK 77
                                                                                                                                                             1;
                                                                                                                          DB 4; Length 832;
                                                                                                                                                           Indels
                                                                                                                       Query Match 3.4%; Score 34.6; DB 4; Pest Local Similarity 9.6%; Pred. No. 0.99; Matches 30; Conservative 153; Mismatches 127;
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LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84773)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84808)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    631 TTCTACGAGAG 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 MYRYSTGTRAS 327
TYPE: DNA
ORGANISM: Homo sapiens
                                ; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
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LENGTH: 1664976
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US-08-916-421B-1/c
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LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a,
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ION: (98120)..(98120)
INFORMATION: n equals a,
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a,
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a,
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LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals
FEATURE:
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LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals
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NAME/KRY: misc feature
LOCAT/KRY: (28259)
OTHER INFORMATION: n equals
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3.4%; Score 34.6; DB 4; Length 1
Best Local Similarity 48.3%; Pred. No. 80;
Matches 97; Conservative 0; Mismatches 104; Indels
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; LOCATION: (1664854)..(1664855)
; CTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t,
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                                                                                      NAME/KEY: misc feature
LOCATION: (68242)..(68242)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (713622)..(713652)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a,
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LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a,
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LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a,
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LOCATION: (1349491)..(1349491)
OTHER INFORMATION: n equals a,
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LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a,
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a,
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LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a,
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THER INFORMATION: n equals a,
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LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a,
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THER INFORMATION: n equals a,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
                   INFORMATION: n equals a,
                                                     LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a,
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RESULT 11
US-09-692-570-1/c
; Sequence 1, Application US/09692570
; Patent No. 679466
; GENERAL INFORMATION:
; APPLICATE BULL et al.
; TITLE OF INVENTION: Januachii
; TITLE OF INVENTION: Januachii
; TITLE OF INVENTION: Januachii
; TITLE REFERENCE: PE27521
; CURRENT APPLICATION NUMBER: US/09/692,570
; CURRENT PILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR PILING DATE: 1997-08-22
; PRIOR PILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO:
                                                                                                                                                  547833 TATACARARATGGATGGGGGTTTGTTACATCAAACATRGTGAGTGAGAGGGAAATCGAAA 547774
547894
                                                                            547834
547953 Addriggadarrangcogararaagaarahaharrriggagagagagagarakaarahah
                                      566 ATGCTGATCCTGAGGAAATAAACTCCATCAGCTCCGCGAGATGATGATCCAGAGAACCGTT
                                                                626 CAAAGTICTACGAGAGTGCTICTGCGAGAAAGAGAAACCGTGACTGCAGAAGAAGAGAGA
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LOCATION: (98239).
OTHER INFORMATION: n equals a, t, C,
FEATURE:
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                                                                                                                                                                                                686 GAGCCATCAATGCAGCCAAAA 706
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NAWE/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or
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LOCATION: (674435)..(674435)
JTHER INFORMATION: n equals a, t,
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LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t,
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ION: (855539)..(855539)
INFORMATION: n equals a, t,
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LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (1119881).
OTHER INFORMATION: n equals a, t,
                                                                                                        PEATURE:
NAME/KEY: misc_feature
LOCATION: (657081).
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a,
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LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a,
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LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a,
      OTHER INFORMATION: n equals a,
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LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a,
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LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals
                          FEATURE:
NAME/KEY: misc_feature
LOCATION: (622708)..(622708)
OTHER INFORWATION: n equals
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LOCATION: (779455)..(779455)
JTHER INFORMATION: n equals
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LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (16338s)..(16338s)
OTHER INFORMATION: n equals a, t, c,
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LOCATION: (559]67)..(559167)
OTHER INFORMATION: n equals a, t, c,
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LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a, t, c,
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LOCATION: (312837)..(312837)
JTHER INFORMATION: n equals a, t, c,
                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a, t,
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LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a, t,
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LOCATION: (191995)..(191995)
JTHER INFORMATION: n equals a, t,
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COCATION: (234187)..(234187)
JTHER INFORMATION: n equals a, t,
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LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a, t,
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LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a, t,
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t,
                                                                                                                                              NAME/KEY: misc feature
LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a, t,
                                                              NAME/KEY: misc_feature
LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a,
FEATURE:
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LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a,
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LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a,
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LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a,
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LOCATION: (600992)..(600992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449 CAGCCAACAAAGGGTATGCTAGTTCAGCCATCCAAACCTTGTTCACTGGACCAGTTAAAG 508
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US-09-270-767-13580
is Sequence 13580, Application US/09270767
js Patent No. 6703491
jg CHURRAL INFORMATION:
jg TAPLICANTH HOMBURGER et al.
jg TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
jg TITLE OF INVENTION: Nucleic 7326-094
jg CURRENT PAPLICANTON NUBER: US/09/270,767
jg CURRENT PAPLICANTON NUBER: US/09/270,767
jg VURBENT PILING DATE: 1999-03-17
jg NUMBER OF SEQ ID NOS: 62517
jg SOFTWARE: Patentin Ver. 2.0
jg SEQ ID NO 13580
jg TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29582, Application US/09270767
Sequence 29582, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT PALLION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SEQ ID NO 29582
LENGTH: 710
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                                                                        Length 1494;
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3.3%; Score 34.2; DB 4; Length 710;
Best Local Similarity 45.9%; Pred. No. 1.2;
Matches 117; Conservative 0; Mismatches 138; Indels
                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            633 CTACGAGAGTGCTTCTGCGAGAAAGAGAGCGTGACTGCA 672
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                                                                        Score 34.4; DB 4;
Pred. No. 1.6;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Drosophila melanogaster
US-09-270-767-29582
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                                                                                 Query Match
Best Local Similarity 59.0%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-09-270-767-29582
US-09-107-532A-2145
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                         547953 AAGTTGGAGATTATGCGGGTATAAGAATAATTTTGGAGAGAGCAATACAATAACATTAA 547894
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                                                                                                                                                          Gaps
                                                     Length 1664976;
                                                         Score 34.6; DB 4; Length 1
Pred. No. 80;
0; Mismatches 104; Indels
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: PS.
SOFTHARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: J112, 1997
ATTONNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1494
SEQUENCE DESCRIPTION: SEQ ID NO: 2145:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   547773 AACTCATAAATAAAGCGTATA 547753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-107-532A-2145/c
; Sequence 2145, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            686 GAGCCATCAATGCAGCCAAAA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2145:
SEQUENCE CHARACTERISTICS:
LENGTH: 1494 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid strandEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7310
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                                                              3.4%;
Best Local Similarity 48.3%;
Matches 97; Conservative
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                                                                                                                                                                                                                                                                        389 AIGCCGAGGICAICTITCCTITCTGTGTACCCATCACCACTICCTGAGTCTACAGTAC 448
                                                                                                                                                                                                                                                                                                                                                                                                                                   449 CAGCCAACAAAGGGTATGCTAGTTCAGCCATCCAAACCTTGTTCACTGGACCAGTTAAAG 508
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APPLICANT: Tai, Joseph Y.
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IGA FC Binding Forms of the Group B TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                       ö
                                                                                                                 Query Match 3.3%; Score 34.2; DB 4; Length 1421; Best Local Similarity 45.9%; Pred. No. 1.8; Matches 117; Conservative 0; Mismatches 138; Indels 0
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COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707

FILING DATE: 05-SEP-1997

CLASSIFICATION NUMBER: US 60/024,707

FILING DATE: 06-SEP-1996

ATORNEY AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 1438.0140001/RWE

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Patent No. 6280738
; ORGANISM: Drosophila melanogaster
US-09-270-767-13580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1029 ACATTCAAAAGAATG 1043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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NAME/KEY:
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Sequence 2973, Ap Sequence 2143, Ap Sequence 2143, Ap Sequence 1119, Ap Sequence 569, App Sequence 64127, A Sequence 101386, Sequence 101386, Sequence 11119, Ap Sequence 11719, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 2527, Ap Sequence 252

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Sequence:

Run on:

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Sequence 1318, Application US/10767795
Publication No. US20040181830A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: WIMBER: US/10/767,795
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT FILING DATE: 2004-01-30
SEQ ID NO 1318
LENGTH: 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCCACGCCCTTTCTTCCATAAGTTGATTTTCTCATCCACTATCCAAGAAAAACGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 39.5%; Score 405.6; DB 17; Length 1471; al Similarity 64.2%; Pred. No. 5.5e-118; 687; Conservative 0; Mismatches 329; Indels 54;
             1 US-09-938-842A-2973

8 US-10-739-930-3743

0 US-10-424-599-3571

0 US-10-742-599-8606

0 US-09-70-423-569

0 US-09-70-423-569

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0 US-09-70-423-569

1 US-09-732-627A-1636

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1 US-09-732-627A-1636

1 US-10-437-963-101386

1 US-10-437-963-49771

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1 US-10-437-963-89684

1 US-10-437-963-86418

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1 US-10-437-963-86418
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US-10-767-795-1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: GOSSYpium hirsutum
Query Match
Best Local Similarity
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US-10-767-795-1318
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Matches
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Sequence 273, App
Sequence 237, App
Sequence 1315, Ap
Sequence 1317, Ap
Sequence 118105,
Sequence 97592, A
Sequence 97591, Ap
Sequence 1320, Ap
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                                                                                                     December 30, 2004, 14:32:07 ; Search time 661 Seconds (without alignments) 8775.732 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-938-842A-273
US-09-938-842A-273
US-09-770-423-237
VS-10-767-795-1316
7 US-10-767-795-1316
6 US-10-424-599-118105
6 US-10-424-599-118105
6 US-10-424-599-118105
7 US-10-767-795-1320
7 US-10-767-795-1320
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1027
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Maximum Match 1008
Listing first 45 summaries
                                                                          nucleic search, using sw model
                                                                                                                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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397.6
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2287.8
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224.2
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ATGCCACGCCTTTTTCCATAAGCTTATTCTCTCCACTACTCTCCAGGACAGGAAACTG 261 AGGGTCCCAGATAAGTTTGTGAGTAAATTCAAGGATGAGCTTTTCGGTTGCTGTTGCACTC 120 262 AGGATACCTGATAACTTTATTAAGAAATTCAGGGATGAGCTTTCTGTTGCTGCCGCTCTC 321 121 ACAGTACCTGATGGTCATGTTTGGCGTGTAGGACTAAGGAAAGCTGACAACAAAATTTGG 180

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TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFRENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US 60/224
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NOS: 5379
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                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Arabidopsis thaliana
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RESULT 3 US-09-938-842A-273

Sequence 273, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
APPLICANT: Harper, Jeff APPLICANT: Wang, Xun APPLICANT: Wang, Yun APPLICANT: Zhu, Tong

RESULT 2 US-09-938-842A-273

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Pred. No. 3.8e-83;
0; Mismatches 3; Indels 0
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APPLICANT: Kricker, Maja
APPLICANT: Kricker, Maja
APPLICANT: Slader, Ted
APPLICANT: Bavis, Keith R.
APPLICANT: Allen, Keith R.
APPLICANT: Hurban, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: LATAIana
FILE REFERENCE: 2028 (PARA-017PRV)
CURRENT APPLICATION NUMBER: 60/178,512
PRIOR APPLICATION NUMBER: 60/178,512
PRIOR APPLICATION NUMBER: 60/178,512
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PRIOR APPLICATION NUMBER: 60/178,512
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                                                               681
   985 GTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGTACGTCTGA
                                                               640 GIICICGAAGICACCGCCIITICGIGICAAIGAGIAIGIGIGA
                                                                                                                                                                                                               Sequence 237, Application US/09770423
Publication No. US20020040490A1
GENERAL INFORMATION:
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COATION: (1)...(426)
COTHER INFORMATION: n = A,T,C or
US-09-770-423-237
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Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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Best Local Similarity 99.0%;
Matches 296; Conservative
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Hamilton, Carol M.
Price, Jennifer L.
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Rameaka, Joshua G.
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                                                                                                                                                                                         US-09-770-423-237/c
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                                                                         APPLICANT: Marper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SARE, AND METHODS OF USE
TITLE OF INVENTION: SARE, AND METHODS OF USE
TITLE OF INVENTION: SOLI-08-24
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-06-24
PRIOR PILING DATE: 2001-06-22
PRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 273
LENGTH: 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     400 CGACCATCATATCTATACAGAGGTTGCATCTGCCATCTGGGTTTGCTGGAAA 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       520 AGGTGCCTCTACAAAGCAGGAGAGCTAAGTTTAGCCAAGGATGGTATGAGTTCACACTC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                385 GAAGATGCCGAGGTCATCTTTCTTTCTGTACCCATCACCACTTCCTGAGTCTACA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 ATGGATTCCGCTCACAACCACTT---CAAACGCGCCCGTTTGTTTGAAGACCTTGAAGAT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          445 GTACCAGCCAACAAAGGGTATGCTAGTTCAGCCATCCAAACCTTGTTCACTGGACCAGTT 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 GAACCAGTGAATAAAGGTTATGGCGGTTCTACAGCCATCCAAAGCTTTTTCAAAGAATCT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAGCTGAAGAGCCAACGCCAACCCCAAAATACCTAAAAAGAGAGGAGGAAGAAGAA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 AAAGCTGAAGA-----AACGCCCAAGGTACTTAAGAAGAGGAGGAAGGAAGAAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 AATCCTAATCCCGAGGAAGTAAACTCTTCAACTCCCGGTGGAGATGACTCAGAGAACCGC 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 AGAGCCGTCAATGCAGCCAAAACATTCGAACCAACAAATCCTTAACTTTAGAGTTGTTCTG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  805 TACCTAAGTGGGATCTCCGGGTTCATCAAAGTCCAGCTTGCGGAGAAACAATGGCCTGTT 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 865 CGATGTCTCTACAAAGCCGGGAGAGCCAAATTCAGTCAAGGATGGTACGAATTCACTCTA 924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 38.7%; Score 397.6; DB 11; Best Local Similarity 76.6%; Pred. No. 1.2e-115; Matches 538; Conservative 0; Mismatches 134;
Sequence 273, Application US/09938842A
Publication No. US20040009476A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Arabidopsis thaliana US-09-938-842A-273
                                   Publication No. US20
GENERAL INFORMATION:
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Sequence 1317, Application US/10767795
Publication No. US20040181830A1
Fublication No. US20040181830A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: APPLICANTON: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REPREBENCE: 38-21(53334)
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT APPLICATION NUMBER: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
LENGTH: 1062
                                                                                                              957 TTACCATCATCATGCTTTGCTGAGAAGTATCTAAGTGGGGGTTTCGGGATTTATTAAACTTCAG 1016
                                                                                                                                                                                  959 TTGAGCTGCTCAGAACCAGAGATTTCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGT 1018
                                                                                                                                                           CTTGCGGA---GAAACAATGGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTC 897
                          404 ACCGTCGTGCTTTGCTGAGAAGCATCTAAGTGGGGTTTCTGGATTCCATTAAACTTCAGC
                                                                              CTTCCTTCTGGGTTTGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAAGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 TGAAGATGATGCTGACATGCGCCTTAGGTGCTATGAAAGTGCTTCTGCCCGAAAGAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGCGGA---GAAACAATGGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 17; Length 1062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C1540_2
US-10-767-795-1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 255.2; DB 17;
Pred. No. 4.6e-70;
0; Mismatches 128;
                                                                                                                                                                                                                                                               AGTCAAGGATGGTACGAATTCACTCTAGAGAACAA 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 24.8%;
Best Local Similarity 73.0%;
Matches 356; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Gossypium hirsutum
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      Sequence 1316, Application US/10767795
Publication No. US20040181830A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53534)B
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQ ID NOS: 117596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ATTTTTAGATATGAAGGAAACTCTGCCTTCAGCGTCTACATTTTCAATTTATCCCACTCT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           603 TTGT-----TTTCTGCGTCTAAAGTTAATAACTGCATGAACTGGAGTGGTGAATCAAT 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAGTACCTGATGGTCATGTTTGGCGTGTAGGACTAAGGAAAGCTGACAAAATTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 GAGATCAATTACCATTCCACCGGTCTCATGGATTCCGCTCACAACCACTTCAAACGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 CGTTTGTTTGAAGACCTTGAAGATGACGAGGTCATCTTTCCTTCTTCTTGTGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           389 ACTGITCCIGACGCICATGITIGGCGIGIAGGAATAAGGAAAGCCGACAACAAGAGTITGG
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                                                                                                                                                                                                                                                                                                                                                                                                                        DB 17; Length 1111;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 287.8; DB 17;
Pred. No. 1.9e-80;
0; Mismatches 267;
                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C1540_3
US-10-767-795-1316
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.0%;
Best Local Similarity 61.3%;
Matches 573; Conservative
                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: GOSSYPium hirsutum
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Gaps

4

602 223 662 283 722 343

782 403 841 463

898 523 928

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Sequence 9015.

Sequence 9015.

Beducation No. US20040123340A1

Bublication No. US20040123340A1

GENERAL INFORMATION:

APPLICANT:

APPLICANT: Feng, Paul C.C.

APPLICANT: Fincher, Karen L.

APPLICANT: Fincher, Karen L.

TILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TILE OF INVENTION: Plants

FILE REFERENCE: 38-21(52274)B

CURRENT FILING DATE: 2001-12-12

PRIOR APPLICATION NUMBER: US 60/255, 619

PRIOR FILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 17880

SEQ ID NO 9015
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Car Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNGS: 38-21 (5.223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 97592
LENGTH: 1740
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ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 118105, Application US/10424599
Publication No. US2004003107241
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihna
APPLICANT: Cao Yongwei
TITLE OF INVENTION: SOy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 118105
LENGTH: 2141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 22.1%; Score 227.2; DB 16; Length Best Local Similarity 71.4%; Pred. No. 6.2e-61; Matches 314; Conservative 0; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_77658C.1 US-10-424-599-118105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-10-424-599-97592
Sequence 97592, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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                             FEATURE:
NAME/KEY: unsure
LOCATION: (1)...(644)
GOTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3828-022-01-K6-E11
US-10-021-323-9015
                                                                                                                                                 Score 174.8; DB 17;
Pred. No. 1.6e-44;
0; Mismatches 223;
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Best Local Similarity 57.1%;
Matches 420; Conservative
TYPE: DNA ORGANISM: GOSSYPium hirsutum
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; Sequence 97591, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION: APPLICANT: La Rosa Thomas J

RESULT 10 US-10-424-599-97591

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Associated With
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                                                       Acid Molecules and Other Molecules
Uses Thereof for Plant Improvement
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TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(35534)B
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQ ID NO 1320
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Pred. No. 6.4e-39;
0; Mismatches 123;
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Best Local Similarity 69.5%; Pred. No. 3.7e-24;
Matches 166; Conservative 0; Mismatches 70;
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_59138C.1
US-10-424-599-97591
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US-10-767-795-1320
APPLICANT: CAO VINUA
APPLICANT: CAO VINUA
APPLICANT: CAO VONGWei
TITLE OF INVENTION: SOY Nucleic Acid Molecul
TITLE OF INVENTION: Plants and Uses Thereof
FILE REPERSNOE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
IENGTH: 628
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Similarity 65.3%;
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Pred. No. 1.2e-20;
0; Mismatches 15; Indels
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9.8%; Score 101; DB 11; Length 20
Best Local Similarity 88.3%; Pred. No. 1.2e-20;
Matches 121; Conservative 0; Mismatches 15; Indels
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PRIOR FILING DATE: 2000-00-27
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
LENGTH: 2000
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Best Local Similarity 88.3%;
Matches 121; Conservative
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US-09-938-842A-2973
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Fublication No. US20040123340A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Peng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Faceler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
GURRENT APPLICANTION NUMBER: US/10/021,323
GURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 7926
LENGTH: 602
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Patent No. US20020160378A1
GENERAL INCOMMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Tan, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REPRESENCE: SCRIP1300-3
FILE REPRESENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
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320 CGTTACTATATTCGTGTTGGCTACTGGTTTTCAGATACGAAGAAATTCTGCTTTC 379
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                                                                        211 CGTTACTCCATTCGCATTGGTTATCTTTTGATTTTTAGATATGAAGGAAACTCTGCCTTC
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US-10-021-323-7926
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Sequence 3743, Application US/10739930
Sequence 3743, Application No. US20040216190A1
Sequence 3743, Application No. US20040216190A1
SEQUENCE OF INVENTION: David K.
TITLE OF INVENTION: WOLLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION: US/10/739,930
CURRENT APPLICATION WUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
SEQ ID NO 3743
LENGTH: 2207
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8.7%; Score 89.6; DB 18; Length 2207;
Best Local Similarity 55.9%; Pred. No. 5.3e-17;
Matches 170; Conservative 0; Mismatches 134; Indels 0;
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, OTHER INFORMATION: Clone ID: GLYMA-23APR03-CLUSTER63260_1

US-10-739-930-3743
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LOCATION: (1)..(2207)
OTHER INFORMATION: unsure at all n locations
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Job time : 664 secs
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 ENRY cedex - PRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clapet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB50ZE05 of Flowers and buds of strain col-0 of Arabidopsis bases.
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07 GR Eb003
19 GR Eb003
68 GR Eb45F
21 701493711
59 GA Ea003
3013 Lambda
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Spermatophyta, Magnollophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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/clone="GSLTFB50ZE05"
/tisque_type="Flowers and bu
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/gene="At3918990"
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Matches 1026; Conservative
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Direct Submitseion

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage:

BP 191 91006 ENYEX cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

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Genoscope members carried out sequencing and annotation: Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.

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Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTILS20ZG12 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).

BX823330
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291
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HTC; GSLT_CDNA.
Arabidopsis thaliana (thale cress)
Exabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eudicots; core eu
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/clone="GSLTLS20ZG12"
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CNSOA6SO 1375 bp mRNA linear HTC 07-FEB-2004 Arabidopsis thaliana Full-length CDNA Complete sequence from clone

DEFINITION

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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : Beqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jailnon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Cleptc C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full Length.
                                                                                                                                                                                                        Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Location/Qualifiers
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/plasmid="pc/vvSPORT 6"
complement(1. .1375)
/gene="At3g18990"
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Pred. No. 1.8e-288;
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BX824523.1 GI:42465662
HTC, GSLT. CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/strain="Col-0"
/db_xref="taxon:3702"
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CNSOAD3Z
Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH45ZCO5 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).
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   93, rue Henri Kouncard.
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                    AFGCCACGCCTTTCTTCCACAAGCTGATTTTCTCATCCACTATCCAAGAAAAACGTCTG
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rue Henri Rochefort 91025 EVRY CEDEX France
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Pred. No. 4.3e-130;
0; Mismatches 67;
                                                                                                       1. 701
/organism="Brassica napus"
/mol type="mRNA"
/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/clone="BN25045C06"
/tissue type="seed"
/clone_lib="BN25"
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Brassica napus
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
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                                                                                               CGTTTGTTTGAAGACCTTGAAGATGAAGATGCCGAGGTCATCTTTCCTTCTTCTGTGTAC
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Unpublished (2003)
Contact: Genoplante
Genoplante
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BN25.045C0F020108 BN25 B:
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CD822418.1 GI:32504358
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AUTHORS
TITLE
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EXELSES: I GI:42473387

HTC; GSLT cDNA.
Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Rabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spernatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 1490)

S Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., WeissenberhJ., and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1081 AACAATATAGGGGAAGGAGATGTATGTGTGTTTGAGCTACTCAGAACTCGGGATTTCGTT 1140
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Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli C., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
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The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). S prime and 3 prime are assembled with Phrap.

However, Www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
                                                                                                                                                                                  Castelli, V., Auryl, M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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(bases 1 to 1420)
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42.9%; Score 441; DB 3; Length 1420;
Best Local Similarity 73.5%; Pred. No. 5.4e-121;
Matches 646; Conservative 0; Mismatches 195; Indels 38; Gaps
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/clone="GSLTPGH45ZC05"
/tissue type="Hormone Treated Callus"
/plasmid="pCWSPORT_6"
complement(1. .1420)
/gene="At1g49480"
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Arabidopsis thaliana
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/strain="Col-0"
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District (18-NOV-2003) Genoscope - Centre National de Sequencage : Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

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http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full
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Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-Length' CDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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0; Mismatches 197;
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/mol type="mRNA"
/strain="Col-0"
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Arabidopsis thaliana (thale cress)
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/clone="GSLTPGH54ZB06"
/tissue_type="Hormone Try
/plaemid="pcWYSPORT" 6"
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URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full_length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 CGTTTCTCCATTCGGATTGGT----TTCAGATACAAAGTTACAGTCTACATTTTCAATTT 340
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                                                                                                                                                    http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195; Indels
                                                                                                                                                                                                                                                                                    /db_xrefe"taxon:3702"
/clone="GSLTPGH13ZB06"
/tissue type="Hormone Treated Callus"
/plasmid="pCMVSPORT_6"
complement(1. .1490)
/gene="At1g49480"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.9%; Score 441; DB 3; I
llarity 73.5%; Pred. No. 5.5e-121;
Conservative 0; Mismatches 195;
                                                                                                                                                                                                                        'organism="Arabidopsis thaliana"
                                                                                                                                                                              Location/Qualifiers
1. .1490
                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="Col-0"
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Best Local Similarity
Matches 646; Conserv
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Light Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedax - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 AGCGICTACAITITCAAITIAICCCACICIGAGAICAAIIACCAITICCACCGGICTCAIG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGAAGAG-----ACGCCCCAAGGTACTTAAGAAGAGAGGGAAGGAAGAAGAAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGACTAAGGAAAGCTGACAACAAAATTTGGTTTCAAGATGGTTGGCAAGAGTTTGTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGACTAAGGAAAGCCAACAACAAAATCTGGTTTCAAGACGGTTGGCAGGAGTTTGTCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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/clone="GSLTLS76ZC03"
/tissue type="Adult vegetative tissue"
/plasmid="pcMvSPORT_6"
complement(1. .880)
/gene="At1g49480"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 410; DB 3; L
Pred. No. 9.9e-112;
0; Mismatches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
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/strain="Col-0"
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                                                                                                                                                                                                                              GATTCCGCACAGATCAGTTCAACAAACGTGCTCGATTGTTGTTGAAGATCCTGAACTCCAA
                                                                                                                                                                                                                                                                                                                               ------CATCGAACCCTGAATCTACTGAA
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                    CGTTACTCCATTCGCATTGCTTATCTTTTAGATATGAAGAAACTCTGCCTTC
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                                                                                                                                                                                              GATTCCGCTCACAACCACTT---CAAACGCGCCCGTTTGTTTGAAGACCTTGAAGATGAA
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BX841843.1 GI:42454500
HTC; GSLT cDNA.
Arabidopsis thaliana (thale cress)
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172 387 232 447 274 507 385

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GTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAGAACCGTGACTGCCGGAAGAAGAG
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bobermatophyta; Megnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicacee; Arabidopsis.
1 (bases I to 589)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Karusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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XhoI"
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                                                                                                      506 AGCCGTCAATGCAG-CAAAACATTCGAACCAACAAATCCTTACTTTAGAGTTGTTCTGCG
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Pred. No. 2.5e-109;
0; Mismatches 2;
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/ecotype="Columbia"
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clone="R2157b09F"
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Best Local Similarity 99.5%;
Matches 403; Conservative
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780 bp mRNA linear EST 01-JUN-2004 204014.pl AtMl Arabidopsis thaliana cDNA clone MPMGp2011014204 CK120978,
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Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 780)
Feilner,T., Immink,R.G.H., Cahill,D.J. and Kersten,B.
Generation of a cDNA expression library from Arabidopsis
inflorescence meristem
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/db_xref="GAB1:95248"
/db_xref="TAB1:95248"
/dl_orne="MPMGp2011014204"
/tissue_type="inflorescence meristem"
/tissue_type="inflorescence meristem"
/tab_host="Rocoli SCS-1/PSE111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGTACGTCTGAA 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2003)
Contact: Birgit Kersten
Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Ihnestr. 73, D-14195 Berlin, Germany
Tel: +49(0)30/84131648
Fax: +49(0)30/84131128
Email: Kersten@molgen.mpg.de
Insert Length: 780 Std Brror: 0.00
Plate: 204 row: 0 column: 14
Seq primer: pQE65;
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/organism="Arabidopsis thaliana"
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the pSPORT vector.
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A1996485.1
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oligo(dT)-primer containing NotI restriction site and a SalI adapter. The main library (plate numbers begin with 1) of 38,000 clones was rearrayed into the sublibrary (plate numbers begin with 201) containing 5,000 putative expression clones. Average insert size is 1 kb. Note: The rearrayed sublibrary (plate numbers begin with 201) was sequenced. Library generation and sequencing was granted in context of GABI-LAPP; data are also accessible at https://gabi.rzpd.de"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 TAAAGGTTATGGCGGTTCTACAGCCATCCAAAGCTTTTTCAAAGAATCTAAAGCTGAAGA
                                                                                                                                                                                                                        GAAAGCTGACAACAAATTTGGTTTCAAGATGGTTGGCAAGAGTTTGTTGACCGTTACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATCTCCGGGTTCATCAAAGTCCAGCTTGCGGAGAAACAATGGCCTGTTCGATGTCTCTA
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                                                                                                                                                                                                Gaps
                                                                                                                                                                                              38;
                                                                                                                                                                 Length 780;
                                                                                                                                                                                              Indels
                                                                                                                                                                Score 396.2; DB 7;
Pred. No. 1.4e-107;
0; Mismatches 183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGAGAAGGACGTCTGTGTGTTTGAGCTGCTCA
                                                                                                                                                                 38.6%;
                                                                                                                                                              Query Match 38.6
Best Local Similarity 72.9
Matches 594; Conservative
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/tissue_type="root"
//dev_stage="4 - 7 weeks"
/dev_stage="4 - 7 weeks"
/dev_stage="4 - 7 weeks"
/clone_lib="A. thaliana, Columbia Col-0, root-1"
/note="Voctor: pSPORT; Site_1: NotI; Site_2: SalI; cDNA
library was derived from untreated root tIssue from
Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks.
Plants were grown in 1:1:1 peat moss/vermiculite/perlite
soil at 22 deg. C +/- 3 deg. C under constant light, and
watered with fertilizer. cDNA synthesis was intilated
using a NotI-oligo(dT) primer. Double-stranded cDNA was
blunted, ligated to SalI adaptors, digested with NotI,
size-selected, and cloned into the NotI and SalI sites of A1996485 108-SEP-1999 701666887 A. thaliana, Columbia Col-0, root-1 Arabidopsis thaliana CDNA clone 701666887, mRNA sequence. Gilliland, D., Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids 11; Brassicales; Brassicaceae; Arabidopsis. 533 736 473 796 856 CTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAAGTCCAGCTTGCGGAGAAACAAT 353 916 GGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTCAGTCAAGGATGGTACGAAT 591 GAACCGTTCAAGTTC-ACGAGAGTGCTTCTGCGAGAAAGAGAAACGTTGACTGCAGAAG 532 AAAGAGAGAGCCATCAATGCAGCCAAAACGTTCGAACCAACAAAACCCTTTCTTCAGAG 1 (Dases 1 to 591)
Chen, J., Momiyama, M., Chan, B., Mooney, M., Carroon, B., Gilliland Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L., and AAAGAGAGAGCCATCAATGCAGCCAAAACGTTCGAACCAACAAACCCTTTCTTCAGAG CTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAAGTCCAGCTTGCGGAGAACAAT GAACCGTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAGAACCG-TGACTGCAGAAG Gaps Contact: David Smoller, Ph.D.
Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte
Pharmaceuticals, Inc.
Hels M77-277-2733
Fax: 314-427-3324
Email: service@genomesystems.com.
Location/Qualifiers .; 7 Length 591; Indele Arabidopsis thaliana Gene Expression MicroArray Unpublished (1999) 37.7%; Score 387; DB 1; I ilarity 99.5%; Pred. No. 7.4e-105; Conservative 0; Mismatches 0; .591
 /organism="Arabidopsis thaliana" /mol_type="mRNA" /ecoType="Col-0" /db_xref="taxon:3702" /clone="701666887" 857 ò

733

673

793 526 853 913

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CD823066
BN25.047120F020109 BN25 Brassica napus CDNA clone BN25047120, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; rosida; eurosida II; Brassicales; Brassicaceae; Brassica. 1 . (bases 1 to 645)
                                                                                                      646
                                                                                                                                                                                                                                                                                                                                                                                                                         914 AATTCACTCTAGAGAACAACTTAGGAGAGAGACGTCTGTGTGTTTGAGCTGCTCAGAA 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                645 AGGAAAGAGAGAGCGGCAATGCAGCCAAAACATTCGAACCAACAAATCCTTACTTTA 586
                                                                                                                                                                                                                                                                                                                                                525 İTGCİĞAĞAAATACCTAAGTĞĞATATCTĞTTTCATCAĞGCTCCAĞCTCĞGTĞAĞAAC 466
Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                           AATGGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTCAGTCAAGGATGGTACG
                                                                                                         674 AAGAAAGAGAGAGAGCCATCAATGCAGCCAAAACGTTCGAACCAACAAACCTTTCTTCA
                                                                                                                                                                                                                                                        CAGAGAACCGTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAGAACCGTGACTGCAG
                                                                                                                                                                                                                               GAGTGGTTCTGCGACCATCCTATACAGAGGTTGCATCATGTATCTTCCTGGGT
                                                                                                                                                                                                                                                                                                              TTGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAAGTCCAGCTTGCGGAGAAAC
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="taxon:3708"
/clone="BN25047120"
/tissue type="seed"
/clone_lib="BN25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="Jet Neuf"
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Best Local Similarity 88.6%;
Matches 412; Conservative
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Brassica napus
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CD823066
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Genoscope - Centre National de Sequencage

BP 191 91006 ENTRY cadex - France

BP 191 91006 ENTRY cadex - France

Email: sequescope.ons.fr, Web : www.genoscope.cns.fr

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out

full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli

V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,

Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis

genome released by MIPS (Wunich Information center for Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1041)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   554 GGAAGAAGAAAATGCTGATCCTGAGGAAATAAACTCATCAGCTCCGCGAGATGATGATC 613
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="Adult vegetative tissue"
/clone lib="Arabidopsis thaliana Adult vegetative tissue
Col-0"
                                                                                                                                                                                                                                                                              BX835682 Arabidopsis thaliana Adult vegetative tissue Col-0
BX835682 Arabidopsis thaliana Adult vegetative tissue Col-0
Arabidopsis thaliana CDNA clone GSLTLS48ZHII 3PKIM, mRNA sequence.
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                                                                                            292 TCACTCTAGAGAACAACTTAGGAGAAGAGGAGGACGTCTGTGTGTTTTGAGCTGCTCAGAACCA
               GGCCTGTTCGATGTCTTACAAAGCCGGAGAGCCAAATTCAGTCAAGGATGGTACGAAT
                                                       TCACTCTAGAGAACAACTTAGGAGAAGGAGACGTCTGTGTGTTTTGAGCTGCTCAGAACCA
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Pred. No. 1.9e-103;
0; Mismatches 114;
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/db xref="taxon:3702"
/clone="GSLTLS48ZH11"
                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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BX835682.1 GI:42529765
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llarity 79.3%;
Conservative
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Unpublished (2004)
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Best Local &
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BX835682/c
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264 IGCCTTCAGCGTCTACATTTTCAATTTATCCCACTCTGAGATCAATTACCATTCCACCGG 323
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                                                                                                                                                                                                                                                                                   61 GAAATTCAGGGATGAACTTTCTGTTGCTGCCGCTCTCACTGTTCCTGACGGTCATGTTTG
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                                                                                                              Gaps
                                                                                                            6
                                                           906;
                                                        Score 362.6; DB 7; Length Pred. No. 1.9e-97; 0; Mismatches 310; Indels
                                                        35.3%;
                                                        Query Match 35.3
Best Local Similarity 64.8
Matches 587; Conservative
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GR Eb0039N17.r GR Eb Gossypium raimondii cDNA clone GR Eb0039N17
3', mRNA sequence.
CO108220.1 GI:48806906
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Gossypium raimondii
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spernatophyta, Varidiplantae, Streptophyta, core eudicots,
rosida, eurosida II, Malvales, Malvaceae, Malvoideae, Gossypium.
1 (bases 1 to 906)
Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
Widall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and
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61 ACCCGGAGAGCCGTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAGAAACGGTTACTG
                                                                                                                                                                                                                                                                                                               GTTTTGCTGAGAAGTACTTAAGTGGGATCTCGGGATTCATCAAGGTCCAGCTCGGGGAGA
                                                                               CAGAAGAAAGAGAGAGCCATCAATGCAGCCAAAACGTTCGAACCAACAAACCCTTTCT
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Global assembly of Cotton ESTs
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, Pax: 520 621 1259
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Plate: 0039 row: N column: 17.
Location/Qualifiers
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612 bp mRNA linear EST 10-JUL-2003
BNIS-020L13F020211 BNIS Brassica napus cDNA clone BNIS020L13, mRNA
Sequence.
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Contact: Genoplante
Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
7el: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
Plant genomics programme 'Genoplante' (http://www.genoplante.com plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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/tissue_type="seed"
/clone_lib="BN15"
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Compugen Ltd
version :
GenCore (c) 1993
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- protein search, using sw model OM protein

December 29, 2004, 13:02:12 ; Search time 98 Seconds (without alignments) 2002.069 Million cell updates/sec Run on:

US-10-088-187A-11 1796 Title: Perfect score:

1 MPRPFFHKLIFSSTIQEKRL......LLRTRDFVLKVTAFRVNEYV 341

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Bed Bed Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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32	3.5	32	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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MEDLINE=22111275; PubMed=12114624;

MEDLINE=22111275; PubMed=12114624;

MILLIAN EASING S., Mylne J.S., Gendall A.R., Dean C.;

"Multiple roles of Arabidopsis VRN1 in vernalization and flowering time control.";

EMBL; AF289051; AAM76972.1; -

EMBL; AF289052; AAM76972.1; -

EMBL; AF289052; AAM76972.1; -

EMBL; AF289055; Pay476973.1; -

EMBL; AF289055; Pay476973.1; -

EMBL; AF289055; Pay476973.1; -

EMBL; AF2890635; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR003340; TF_B3.

EMBL; AF028053; B3; 2.

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EMBL; AF02182; B550663; B3; 2.
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales, Brassicaceae; Arabidopsis.
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                                                                                                                                           01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                              341 AA
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Best Local Similarity 100.
Matches 341, Conservative
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Gaps

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RESULT Q6R2U8 ID Q6

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59 IWFQDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSA--HNH 116
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EMBL, AN356368; AAQ55453.1; -.

InterPro; IPR00340; TF_B3.

PROSITE; PS50863; B3; 2.

SEQUENCE 329 AA; 37931 MW; BFF71D55ADE2655A CRC64;
                                                Kwon S.-J., Park B.-S., Kim S.-Y., Choi H.-S., Lee M.-C., Kim J.-S.,
Lee S.-I., Lim K.-B., Kim J.-A., Lee M.-R., Jin Y.-M., Kim D.,
Kim H.-I.;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Reduced vernalization response Last
Brassica campestris (Field mustard).
Brassica campestris (Field mustard).
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids; NCBL TaxID=3711;
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                                                                                                                                                                                                                                                                                                                                                                                     13; Indels
                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                      "Brassica rapa Kwonsim VRN1 mRNA.";
Submitred (DEC-2203) to the EMBL/GenBank/DDBJ databases
EMBL; AYS17929; AAR91199.1, -
SEQUENCE 329 AA; 38058 MW; A24ADB91433459BB CRC64;
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2e-107;
14;
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84.2%; Score 1513; DB 2;
Best Local Similarity 85.1%; Pred. No. 1e-107;
Matches 296; Conservative 13; Mismatches 13;
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85.1%; Pred. No. 2e-1
ive 12; Mismatches
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Matches 296; Conservative
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Qevoje,
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02-MAR-2004 (TrENBLrel. 27, Created)
02-MAR-2004 (TrENBLrel. 27, Last sequence update)
02-MAR-2004 (TrENBLrel. 27, Last sequence update)
Reduced vernalization response 1.
Brassica campestris (Field mustard).
Brassica campestris (Field mustard).
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
NCBL_TAXID=3711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
NCBI_TaxID=3711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
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Kwon S.-J., Park B.-S., Kim S.-Y., Choi H.-S., Lee M.-C., Kim J.

Lee S.-I., Lim K.-B., Kim J.-A., Lee M.-R., Jin Y.-M., Kim D.,

Kim H.-I.;

Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AY517929, AA82199.1;

InterPro; IPR003340; TF_B3.

Pfam; PF02362, B3; 2.

PROSITE; PS50863; B3; 2.

SEQUENCE 329 AA; 38058 MW; A24ADB91433459BB CRC64;
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84.2%; Score 1513; DB 2; Length 329;
Best Local Similarity 85.1%; Pred. No. 1e-107;
Matches 296; Conservative 13; Mismatches 13; Indels 2
                                  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Reduced vernalization response 1.
Brassica campestris (Field mustard).
QGWYEFTLENNLGEGDVCVFELLRTRDFVLKVTAFRVNEYV
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301
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99.1%;
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                                                        01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2003 (TrEMBLrel. 25, Gb|AAD43153.1.
                                                                                                                                                                                                                                                                                                                   and BAC clones.";
Res. 7:217-221(2000).
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                          PRELIMINARY;
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                                                                                                                                                                                                 NCBI_TaxID=3702;
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233
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                                                       FKRARLFEDLEDEDAEVIFPSSVYPSPLPESTVPANKGYASSAIQTLFTGPVKAEE--PT 174
                                                                                                                          PTPKIPKKRGRKKKNAD-PEEINSSAPRODDPENRSKFYESASARKRTVTAEERERAINA 233
                                                                                                                                                                                              AKTFEPTNPFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQLAEKQWPVRCLYK 293
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                                                                                                                                            162 QTSKVPKKRGRKKKNADHPEEVNSSAPRDDDPESRSKFYESASARKGTVNAEREREAAVNA
                                                                                                                                                                                                                   61 IWFQDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVCIYNLPOSEINYHSTGLMDSASHNNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 QTSKVPKKRGRKKKNADHPEEVNSSAPRDDDPESRSKFYESASARKGTVNAEERERAVNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 FKRPRLFEDLEDEDAETLHTT-------ASAIQSFFTGPVKPERATPT
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Kwon S.-J., Park B.-S., Kim S.-Y., Choi H.-S., Lee M.-C., Kim J.-S.,
Lee S.-I., Lin K.-B., Kim J.-A., Hong K.-Y., Lee M.-R., Jin Y.-M.,
Kim D., Kim H.-I.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                              AGRAKFSQGWYEFTLENNLGEGDVCVFELLRTRDFVLKVTAFRVNEYV 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY356368; AAQ55453.1; -. SEQUENCE 329 AA; 37931 MW; BFF71D55ADE2655A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAR-2004 (TrEMBLrel. 27, Last sequence update) 02-MAR-2004 (TrEMBLrel. 27, Last annotation update) Reduced vernalization response 1.
Brassica campesris (Field mustard).
                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAR-2004 (TrEMBLrel. 27, Created)
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Matches 296, Conservative
                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3711;
                                                                                                                                                                                                                                                              294
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AAQ55453;
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169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 AINAAKTFEPTNPFFRVVLRPSYLYRGCIMYLPSGPAEKYLSGISGFIKVQLAEKQMPVR 289
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                                                                                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety TAC and BAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N. 1.
SEQUENCE FROM N. 3 ato S., Nakamura Y., Asamizu E., Tabata S.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AP000735; BAB01695.1; -.
GO, GO:0003677; P:DNA binding; IEA.
GO; GO:0006357; P:PROJALion of transcription, DNA-dependent; IEA.
InterPro; IPR003340; TF_B3.
InterPro; IPR003340; TF_B3.
PROSTIE; PS50863; B3; 1.
PROSTIE; PS50863; B3; 1.
SEQUENCE 230 AA; 26219 MW; B96A826B384C9F3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLYKAGRAKFSQGWYEFTLENNLGEGDVCVFELLRTRDFVLKVTAFRVNEYV 341
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Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.
Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLYKAGRAKFSQGWYEFTLENNLGEGDVCVFELLRIRDFVLKVTAFRVNEYV
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                                                                     Last sequence update)
Last annotation update)
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Pred. No. 1e-83;
0; Mismatches
230 AA
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                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress)
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Created)
Last sequence update)
Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 103; Conservative
                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                      P0022F10.13 protein.
Name=P0022F10.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=39947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nguyen M., Karlin.Neumann G., Southwick A., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.Y., Narneaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY0428689 AAK6808.1;
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                    3 MDSAQNQFNKRARLFEDPELKDAKVIYPSN-----PESTEPVNKGYGGSTAIQSFFK-E
                                                                                                                                                                                                                                                                      113 ERAVNAAKTFEPTNPYFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKLQLGEKQWP
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                                                                                                                                                                                                                                                         168 VKAEEPTPTPKIPKKRGRKKKKNADPEEINSSAPRDDDPENRSKFYESASARKRTVTAEER
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein F13F21.8,
Name=F13F21.8,
Arabidopsis thaliana (Mouse-ear cress),
Eukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids 11; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                             Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
ENBL, ACOOTS04, AnD43153.1;
PIN: B96531, E96531.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IRRO3340; TF_B3.
PROSITE; PS05063; B3; 1.
PROSITE; PS05063; B3; 1.
SEQUENCE 226 AA; 25850 MW; CB902C011E446A67 CRC64;
                                                                                                                                                                             12;
                                                                                                                                                   Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.4%; Score 942; DB 2; Length 226; 80.8%; Pred. No. 3.5e-64;
                                                                                                                                                                            18; Indels
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                                                                                                                                                   52.7%; Score 946; DB 2;
81.2%; Pred. No. 1.7e-64;
                                                                                                                                                                             14; Mismatches
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Matches 189; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 AA
                                                                                                                                                              Best Local Similarity 81.2
Matches 190; Conservative
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As Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Rasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Rasaki T., Matsukawa M., Arikawa K., Chiden Y., Hayashi M., Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M., Ra Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., Ra Hijishita S., Honda M., Ichikawa Y., Idohuma A., Iijima M., Ikeda M., Rah Hijishita S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K., Rasaswa W., Katagiri S., Kikuta A., Kobayashi N., Kono I., Machara T., Mizuno H., Mizubayashi T., Mukai Y., Nachita K., Machara T., Mizuno H., Mizubayashi T., Mukai Y., Ramagashi H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M., Song U., Takazaki Y., Terasawa K., Teuji K., Rah Maki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Yang H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y., Aran Guenome sequence and structure of rice chromosome I.";

Namik A., Namagata H., Sugus J., Hahn J.H., Kim H.I., Eun M.Y., Aran Guenome sequence and structure of rice chromosome I.";

Namik A., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Maki K., Ma
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287
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                                                                   113 A---HNHFKRARLFEDLEDEDA------EVI----FPSSVYP-----SPLPES
228 ERAINAAKTFEPTNPFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQLAEKQWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartojdeae; Oryzeae; Oryza.
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303 WYEFTLENNLGEGDVCVFEL
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SSAPRDDDPENRSKFYESASARKRTVTAEERERAINAAKTFEPTNPFFRVVLRPSYLYRG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 VYPSPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPK--KRG-----RKKKN 189
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                          302 FMMRPPTGFSRQHLPRERIDVVLRDPGGKVWSV--LYIPNTRDRLSRGWCAPARGNCLEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantes, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR003340; TF_B3.
Pfam; PF02362; B3; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.0%; Score 251.5; DB 2; Length 750; 26.9%; Pred. No. 1.5e-10; ive 55; Mismatches 134; Indels 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buell R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
1-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Putative auxin response factor.
Name-OSJNBb0111B07.22;
                                                                                                                                                                                                                                                                                                                                             750 AA
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GDYCVPELVAAAEF--RVHIFRVVE 382
                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                 GDVCVPELLRTRDFVLKVTAFRVNE
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Gramene; Q851V0; -.
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                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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hes 86; Conserv
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197
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 EDLEDEDAEVIFPSSVYPSPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPKKR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 VIDNCKKKKKTEHASSEDDQ------ETPTAEVHRMKVEEMVRAIHS-----NHPV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 GRKKKNADPEEINSSAPRDDDPENRSKFYESASARKRTVTAEERERAINAAKTFEPTNPF 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRVVLRPSYLYR-GCIMYLPSGFAEKYLSGISGFIKVQLAEKQWPVR-CLYKAGRAKFSQ 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 QNMQGDPIEILSCSDEHLRAQSLTTERQNQ--------PEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 PFHKLIPSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKIWFQDG
                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton I.L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salaberg S.L., Fraser C.M.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cramene; Q851V5; -... EMBL/GenBank/DDBJ databases.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IFR003340; TP_B3.
Pfam; PF02362; B3; 5.
PROSITE; PS50863; B3; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 246; DB 2; Length 10;
; Pred. No. 5.9e-10;
60; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Buell R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                             24, Last sequence update) 25, Last annotation update)
                                                                                                                                                  1029 AA
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                                                                                                                                                                                                     Created)
                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                             Putative auxin response factor.
Name=OSJNBb0111B07.17;
698 WRQFAGDNRLVAHDVCLFEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.7%;
23.8%;
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Matches 74; Conservative
                                                                                                                                                  PRELIMINARY;
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GWRKFTRDNEL
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QBRYD1
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Smith R.;

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AAQ89626;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 HNHFKRARLFEDLEDEDAEVIFPSSVYPSPLPESTVPANKGYASSAIQTLFTGPVKAEEP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 AINAAK-TFEPTNPFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQLAEKQWPV 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 PGFH-------NRLVIPRKFSTHCKRKLPQIVTLKSPSGVTYNVGVEEDDEKTMAFR 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 PFFHKLIFSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNK-IWFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 TGYEQEEHINSDIDTASAQL------PVISPTSTVRVSEG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 TPTPKIP----KKRGRKKKNADPEEINSSAPRDDDPENRSKFYESASARKRTVTAEERER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 RC-LYKA-GRAKFSQGWYEFTLENNLGEGDVCVFELL--RTRDFVLKVTAFRVNE 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLEEL: 10, Last Sequence update)
05-JUL-2004 (TrEMBLEEL: 27, Last annocation update)
115B16.18 protein (Hypothetical protein AT4g01580).

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Etreptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; coreids; eurosids 11; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AJ441117, CAD29616.1, -.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82;
                                                                                                                                                                                                                                                                                                                                 :
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Sessa G., Carabelli M., Ciarbelli A.R., Ruzza V., Steindler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 24.5%; Pred. No. 4.5e-10; Local 87; Conservative 57; Mismatches 129; Indels
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                                                                                                                                                                                                                                                                                                                                    Sessa G., Carabelli M., Ciarbelli A.R., Ruzza V., Steinc
Ruberti I.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003340; TF_B3.
Pfam; PP02362; B3; 2.
PROSITE; PS50863; B3; 2.
SEQUENCE 337 AA; 38760 MW, 8CA7E445600DA3CB CRC64;
                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.3%; Score 239; DB 2; 24.5%; Pred. No. 4.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 AA
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                                                                                                 Auxin response factor 36.
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                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
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Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplande, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                              Cheuk R., Chen H., Kim C.J., Shinn P., Carninci P., Hayashizaki Y., Shihda J., Kaniya A., Kawai J., Narusaka M., Sakurai T., Satou M., Seki M., Shinnzaki K., Ecker J.R.; Seki M., Shinnzaki K., Ecker J.R.; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; T02015; T02015.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR008972; Cupredoxin.
InterPro; IPR003340; TF_B3.
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"Arabidopals ORP clones.",
"Arabidopals ORP clones.",
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BT010604, AAQ895626.1;
ERMEL; BT010604, AAQ895626.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 190;
                                                                                                                                                                                                                                                                                                     [5]
SEQUENCE FROM N.A.
Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF104919, AAG72857.1; -.
EMBL; BT010604; AAQ8656.1; -.
EMBL; AL161492; CAB77728.1; -.
                     the EMBL/GenBank/DDBJ databases.
                                                                                                       R.;
(NOV-1998) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
12.8%; Score 229; DB 2;
Best Local Similarity 33.3%; Pred. No. 1.2e-09;
Matches 53; Conservative 25; Mismatches 51.
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T., Smith F
(NOV-1998)
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Submitted
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227 DVETTPNQQLVISPPVDNELEDLIDIDLDFDIDKILNPLLVASHTGYEQEEHINSDIDTA 286
                                                                                                                                          | : |: :: | : | : | 328 AGSNKKALSL-----AKRAISPDG--FLVFMKRSHVVSKCFLTIFYKWCVKNMLITR 377
                                                                                                                                                                                                                                                                                                                                                                                             378 QEVVMQVDQTKWEMKFNIFGARGSGGISTGWKKFVQDNNLREGDVCVFEPANSETKPLHL 437
                                                                                                                                                                                                                              215 ASARKRIVIAEERERAINAAKIFEPINPFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGIS 274
                                                                                                                                                                                                                                                                                                                                                           275 GFIKVQLAEKQWPVRC-LYKA-GRAKFSQGWYEFTLENNLGEGDVCVFELL--RTRDFVL 330
                                                                                                 164 FTGPVKAEEPTPTPKIP-----KKRGRKKKNADPEEINSSAPRDDDPENRSKFYES 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: December 30, 2004, 06:10:40 Job time : 100 secs
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                                                                                                                                                                                                                                                                                       66 QEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINY--------HSTGL- 109
                                                                                                                                                                                                                                                                                                                             90 SEFAEAKSIEEGHFLLFEYKKNSSFRVIIFNASACETNYPLDAVHIIDSDDDVIEITGKE 149
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                                                                                                                                                                                                   | ||: ||::| :||:|| :|| 30 FFKLVLPSTWKDKRIPPRFVKLQGSKLSEVVTLVTPAGYKRSIKLKRIGEEIWFHEGW 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 RL-------FEDLEDEDARVIFPSSVYPSPLPESTVPANKGYASSAIQTL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 VPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNK-IWFQDGWQEFVDRYSIRIGYLL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mayer K.F.X.;
                                                                                                                                                       6 PHKLIFSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKIWFQDGW
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                                                                                              30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein F17MS.40 (Hypothetical protein AT4g33280).
Name=F17MS.40; Synonyme=AT4g33280,
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; edicotyledons; core eudicots; rosids; elemental in; Brassicales; Brassicaceae; Arabidopsis.
NCBL TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Bevan M., Rose M., Hempel S., Entian K.-D., Hoheisel J., Mewes H.W.,
Mannhaupt G., Mayer K.P.X., Schueller C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO13678; CAB30465.1; -..
EMBL; ALO13678; P.DNB binding; IEA.
GO; GO:0003677; P:DNB binding; IEA.
GO; GO:0003577; P:DNB binding; IEA.
GO; GO:0005357; P:CAB3141ion of transcription, DNA-dependent; IEA.
PROSITE; PSS0863; B3; 2.
PROSITE; PSS0863; B3; 2.
PROSITE; PSS0863; B3; 2.
PROSITE; PSS0863; B3; 2.
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                                 Length 190;
                                                                                              51; Indels
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Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 MDSAHNHFKRAR-----LFEDL-----EDEDAEVI 134
                          ch 12.8%; Score 229; DB 2; 1 Similarity 33.3%; Pred. No. 1.2e-09; 53; Conservative 25; Mismatches 51
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                          Query Match
Best Local Similarity
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THIS PAGE BLAWK (USPIO)

5.1.6 Compugen Ltd. version : GenCore (c) 1993 Copyright

OM protein - protein search, using sw model

December 29, 2004, 19:00:56; Search time 23 Seconds (without alignments) 1426.518 Million cell updates/sec Run on:

US-10-088-187A-11 1796 I MPRPFFHKLIFSSTIQEKRL......LLRTRDFVLKVTAFRVNEYV 341 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* Database :

piri:* pir2:* pir3:* 4.0.6.4 .....

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
	Score	ery	Length	DB		Description
-	946	52.7	226	2	E96531	hypothetical prote
7	229	12.8	190	7	T02015	
m	227.5	12.7	461	~	T05979	_
4	182.5	10.2	308	~	T49920	
2	172	9.6	286	7	H84537	_
9	172	9.6	389	~	T04786	_
7	161.5	9.0	352	7	T05106	_
80	145	8.1	344	~	T05104	_
6	141.5	7.9	210	~	D96531	
10	141	7.9	283	7	T45871	
11	140.5	7.8	461	~	T05101	-4
12	137.5	7.7	490	~	T01545	
13	134	7.5	512	7	T05107	hypothetical prote
14	133.5	7.4	984	~	G86393	protein T24P13.6
15	133.5	7.4	1440	~	C84639	hypothetical prote
16	133	7.4	899	~	H84639	
17	132	7.3	493	~	T05105	
18	_	9.9	478	~	T05102	
19	116.5	6.5	851	7	F84639	
20	111	6.2	608	N	AE2531	
21	110.5	6.2	1021	~	T05108	hypothetical prote
22	107.5	6.0	2783	Н	A41948	v
23	104	5.8	497	~	T14433	reproductive meris
24	102.5	5.7	134	~	E86301	F19K19.7 protein -
25	102.5	5.7	232	~	T22698	hypothetical prote
26	101.5	5.7	243	~	JN0788	tonB protein - Kle
27	101.5	5.7	482	~	T22981	hypothetical prote
28	101		1507	~	S.	alpha-2-macroglobu
. 29	66	5.5	298	7	T37251	homeobox protein c

hypothetical prote hypothetical prote	hypothetical prote TonB protein [impo	hypothetical prote hypothetical prote	hypothetical prote	MG032 homolog B01_	hypothetical prote	translation elonga	hypothetical prote	probable secreted	hypothetical prote	heat shock protein
• •										
T29657 T26819	T15269 AD0267	T05109 A84767	T06310	S73444	T45894 T16740	838003	T00948	C81357	G84639	T09882
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586	1082	525 297	852	673	932	1008	599	541	682	823
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8 8 8 8	97.5 97	97 96.5	96	95	95	94	92.5	92	92	95
30	32 33	34 35	36	38	0. 4 0. C	41	42	43	44	45

## ALIGNMENTS

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hypothetical protein F13F21.8 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Sate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Sacession: E96531
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hujans, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Ttlle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: E96531
A; Accession: E96531
A; Schwarz, M.; MulD:21016719; PMID:11130712

A, Molecule type: DNA

A;Residues: 1-226 <STO> A;Cross-references: UNIPROT:Q9XIB5; GB:AE005173; NID:g5430753; PIDN:AAD43153.1; GSPDB:GR

C, Genetics:

A; Gene: F13F21.8 A; Map position: 1

Gaps 12; 52.7%; Score 946; DB 2; Length 226; 81.2%; Pred. No. 3.3e-69; ive 14; Mismatches 18; Indels Best Local Similarity 81.2* Matches 190; Conservative Query Match Best Local Similarity

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110 MDSAHNHF-KRARLFEDLEDEDAEVIFPSSVYPSPLPESTVPANKGY-ASSAIQTLFTGP 167 55 3 MDSAQNQFNKRARLFEDPELKDAKVIYPSN-----PESTEPVNKGYGGSTAIQSFFK-E à g

168 VKAEEPTPTPKIPKKRGRKKKNADPEEINSSAPRDDDFENRSKFYESASARKRTVTAEER 227 Š

56 SKAEE---TPKVLKKRGKKKKNPNPEEVNSSTPGGDDSENRSKFYESASARKRTVTAEER 112 셤

ERAINAAKTFEPTNPFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQLAEKQWP 287 228 113 δ 셤

VRCLYKAGRAKFSQGWYEFTLENNLGEGDVCVFELLRTRDFVLKVTAFRVNEYV 341 VRCLYKAGRAKFSQGWYEFTLENNIGEGDVCVFELLRTRDFVLEVTAFRVNEYV 226 288 ò 요

RESULT T02015

173

hypothetical protein T15B16.18 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49920
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, April 2000
A;Reference number: 224490
A;Accession: T49920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:091XE1; EMBL:AL353994; GSPDB:GN00063; ATSP:F17114.30
A;Experimental source: cultivar Columbia; BAC clone F17114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
       328 AGSNKKALSL-----AKRAISPDG--FLVFMKRSHVVSKCFLTIPYKWCVKNMLITR 377
                                                                                                                           275 GFIKVQLAEKOWPVRC-LYXA-GRAKFSQGWYEFTLENNLGEGDVCVFELL--RTRDFVL 330
                                                                                                                                                                   64 --GWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSAHNHFKRAR 121
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10.2%; Score 182.5; DB 2; Length 308;
Best Local Similarity 24.6%; Pred. No. 3.1e-07;
Matches 83; Conservative 51; Mismatches 145; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 33/3; 132/1; 231/3
C;Superfamily: Arabidopsis thaliana hypothetical protein F17114.30
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                                                                                                                                                                                                                                                                                                                                                              438 NVYIFRGEE 446
                                                                                                                                                                                                                                                                                  331 KVTAFRVNE 339
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A;Molecule type: DNA
A;Residues: 1-308 <BEV>
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H84537
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Typothetical protein F17M5.40 - Arabidopsis thaliana
C;Species: Azabidopsis thaliana (mouse-ear cress)
C;Species: Azabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1399 #sequence_revision 30-Apr-1399 #text_change 09-Jul-2004
C;Accession: T05979
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15263
A;Rosesion: T05979
A;Molecule type: DNA
A;Residues: 1-461 - 8EEV>
A;Cross-references: UNIPROT:Q9SZA5; EMBL:AL035678; GSPDB:GN00062; ATSP:F17M5.40
A;Experimental source: cultivar Columbia; BAC clone F17M5
C;Genetics: A;Gene: ATSP:F17M5.40
A;Map position: 4
A;Introns: 37/3; 328/1; 362/3
C; Accession: T02015
R; Stoneking, T.; Smith, R.
submitted to the BMBL Data Library, November 1998
submitted to the BMBL Data Library, November 1998
A; Description: The sequence of A. thaliana T15B16.
A; Recession: T02015
A; Accession: T02015
A; Residues: L-190 <STO>
A; Residues: 1-190 <STO>
A; Residues: 1-190 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 MDSAHNHFKRAR----LPEDL-----EDEDAEVI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.8%; Score 229; DB 2;
33.3%; Pred. No. 2.8e-11;
tive 25; Mismatches 51;
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A; Reference number: A84420; MUID:20083487; PMID:10617197 A; Accession: H84437 A; Accession: H84437 A; Accession: H84437 A; Catus: preliminary A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Conservative type: DNA A; Conservative type: DNA A; Molecule type: DNA A; Conservative type: DNA A; Molecule type: DNA A; Conservative type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type:	Db 130 LSSEDTDTGAKSEMKNTVPEGRDKGKSKVEVVEDSDDDEEEDSVYSESSEETB 182  Qy 149 VPANKGYASSAIQTLFTGPVKAEEPTPTRIEKKRGRKK
121 130 181 155 237 295 248	RESULT 7 T05106 hypothetical protein F28M70.170 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Bate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C;Accession: T05106 R;Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, November 1998 A;Recession: T05106 A;Molecule type: DNA A;Residues: 1-352 aBEV> A;Cross-references: UNIPROT:Q9SB80; EMBL:AL031004 A;Residues: 1-352 aBEV> A;Cross-references: UNIPROT:Q9SB80; EMBL:AL031004 A;Residues: 26/3; 125/1; 166/3 A;Mote: F28M20.170 C;Superfamily: Arabidopsis thaliana hypothetical protein F28M20.180
TESULT 6 TOATOL TOATOL TO A TABLIDADE THAILAND TOATOL TOATOL TO A TABLIDADE THAILAND TOATOL TOATOL TOATOL TOATOL TOATOL TOATOL TOATOL TOATOL C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C; Date: 23-Apr-1999 #sequence Database, Rebruary 1999 T; Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Hoheisel, J.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1999 A; Reference number: 215384 A; Accession: T04786 A; Molecule type: DNA A; Resentine: 1-389 ** BEV- A; Resentine: 1-389 ** BEV- A; Cross references: UNIPROT: 095205; EMBL; AL035521 A; Cross references: UNIPROT: Columbia; BAC clone F10M10 C; Genetics: A; Hap position: 4 A; Note: F10M10.170	Query Match         9.0%;         Score 161.5;         DB 2;         Length 352;           Best Local Similarity         20.1%;         Pred. No. 1.9e-05;         Indels 123;         Gaps 15;           Matches         69;         Conservative         49;         Mismatches 102;         Indels 123;         Gaps 15;           QY         5         FFHKLIFSSTIOEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKI 59
Query Match         9.6#; Score 172; DB 2; Length 389;           Best Local Similarity 21.0#; Pred. No. 3.1e-06;         All Second State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of St	Qy 240 TNPFRVULRPSYLYRGCIMYLPSGFAEKYLSGIS-GFIKVQLAEKQWPVRC-LYKA 294  Db 148 DLTCFSQSYTASNLTRD-LVGIPRDFAKRYGLNIGRHEIVLMDEEGNTWESEVKSYKS 204  Qy 295 GRAKFSQGWYETLENNLGEGDVCVFELLRTRDFVLKVTAFRV 337

210;

Length

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83 VWFEKGWRD-
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Matches 66; Conserv
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  Query Match
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RiTheologis, A.; Backer, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Kazo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Huthors: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A.Reference number: A86141; MUD:21016719; PMID:11130712
A.Status: preliminary
A.Molecule type: DNA
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A,Cross-references: UNIPROT:Q9XIB4; GB;AE005173; NID:g5430754; PIDN:AAD43154.1; GSPDB:GN
C;Accession: T05104
R;Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes, Bubmitted to the Protein Sequence Database, November 1998
A;Reference number: Z15398
A;Reference number: Z15398
A;Reference number: Z15398
A;Residues: T05104
A;Residues: 1-344 cBEV>
A;Residues: 1-344 cBEV>
A;Cross-references: UNIFROT: 081781; EMBL: AL031004
A;Experimental source: cultivar Columbia; BAC clone F28M20
C;Genetics:
A;Map position: 4
A;Introns: Z6(3; 120/1; 144/1; 185/3; 224/1; 275/3
A;Note: F28M20.150
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                    88;
                                                                                                                                                                                                                                                                                                          Length 344;
                                                                                                                                                                                                                                                                                                       / Match 8.1%; Score 145; DB 2; Length 34. Local Similarity 23.6%; Pred. No. 0.0004; Los 88; Conservative 51; Mismatches 146; Indels
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A, Map position: 1
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hypothetical protein F28M20.120 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C;Accession: T05101 R;Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes,
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45871
R;Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, N.;Reference number: Z23016
A;Reference number: Z23016
A;Reference number: T45871
A;Status: preliminary
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-283 <BLO>
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A;Experimental source: cultivar Columbia; BAC clone F4P12
; Score 141.5; DB 2;
; Pred. No. 0.00039;
24; Mismatches 39;
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19.8%; Pred. No. 0.00064;
iive 49; Mismatches 127;
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      7.9%;
                                                                   43; Conservative
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                                                                                                                                                                                                                                                                                                                                                               57 NKIWFQDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINY----HSTGLMD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                  112 SAHNHFKRARLFEDLEDEDAEV----IFPSSVYPSPLPESTVPANKGYASSAIQTLFTG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 PVKAEBPTPTPKIPKKRKKKKKNADPEBINSSAPRDDDPENRSKFYBSAS---ARKRTVT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KRSGFSKGR---HEIVLMNEEGKSWESEVKSYMSGAVYLVGGWTTF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 AEERERAINAAKTP----EPTNPFRVVURPSYLYRGCIMYLPSGFAEKYLSGISGFI-- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 -KVQLAEK---QWPVRCLYXAGRAKFSQG---WYEFTLENNLGEGDVCVFELLR----- 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 PFQPLLPGFQS-----NLKIPVNYFSEHIEGKHEGKTVTLRTDASERTWEVKMEGHR--- 65
                                                                                                                                                                                                                                                                                           5 FFHKLI--FSSTIQEKRLRVPDKFVSKF---KDELSVAVALTVPDGHVWRV---GLRKAD 56
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                             95;
                                                                                                                                                                                     Superfamily: Arabidopsis thaliana hypothetical protein F28M20.180
                                                                                                                                                                                                                             Length 461;
                                                                                                                                                                                                                                       Local Similarity 21.5%; Pred. No. 0.0014; Indels es 81; Conservative 50; Mismatches 151; Indels
                A;Reference number: 215398
A;Accession: T05101
A;Accession: T05101
A;Accession: T05101
A;Cossion: 176510
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A;Experimental source: cultivar Columbia; BAC clone F28M20
C;Genetics:
A;Map position: 4
A;Ntrons: 26/3; 125/1; 163/3; 245/3; 316/3
A;Note: F28M20 C;Superfamily: Arabidopsis thaliana hypothetical protein F2
submitted to the Protein Sequence Database, November 1998
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                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                             7.8%; Score 140.5;
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Best Local S
Matches 81
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hypothetical protein A_IG005110.15 - Arabidopsis thaliana
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Species 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01545
R;Andrews, S
Submitted to the EMBL Data Library, July 1997
A;Pescription: The sequence of A. thaliana IG005110.
A;Reference number: 214347
A;Accession: T01545
A;Reference number: 214347
A;Accession: T01545
A;Residues: 1-490 <AND>
A;Residues: 1-490 <AND>
A;Residues: 1-490 <AND>
A;Cross-references: UNIPROT:023076; EMBL:AF013293; NID:g2252823; PID:g2252835
A;Genetics:

A,Map position: 4 A,Introns: 112/3; 216/1; 256/3; 391/3 A,Note: A_IG005110.15 C,Superfamily: Arabidopsis thaliana hypothetical protein F28M20.180

22 VPDKFVSKF---KDELSVAVALTVPDGHVWRVGLRKADNKIWFQDGWQEFVDRYSIRIGY 78 Gaps 65; Indels Query Match 7.7%; Score 137.5; DB 2; Best Local Similarity 23.4%; Pred. No. 0.0026; Matches 81; Conservative 42; Mismatches 158;

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hypothetical protein F28M20.180 - Arabidopsis thaliana (\$\frac{5}{2}\) Species Arabidopsis thaliana (\$\text{mouse-ear}\) cress)
C;\text{5}\) C;\text{5}\) C;\text{5}\) As \$\text{5}\] C;\text{5}\) As \$\text{5}\] C;\text{5}\] C;\text{5}\] C;\text{5}\] C;\text{5}\] C;\text{5}\] C;\text{5}\] C;\text{5}\] C;\text{5}\] C;\text{5}\] C;\text{5}\] C;\text{5}\] C;\text{5}\] C;\text{5}\] May By \(\text{5}\), \(\text{6}\) A;\text{6}\] By May By \(\text{6}\), \(\text{6}\) A;\text{6}\] C;\text{6}\] Movember 1998
A;\text{Reference number: 215398}

A;Introns: 26/3; 184/3; 322/3; 402/3 A;Note: F28M20.180 C;Superfamily: Arabidopsis thaliana hypothetical protein F28M20.180 A;Accession: T05107
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/ Match 7.5%; Score 134; DB 2; Length 512; Local Similarity 19.9%; Pred. No. 0.0053; Los 69; Conservative 47; Mismatches 111; Indels 120; Query Match

1 MPRP----FFHKLIFSSTIQEKRLRVPDKFV-SKFKDEL-SVAVALTVPDGHVWRVGLRK

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106 166 220 154 -------KKRARKETESSSDKSYLVAHVTPSSLLRDNMCVLSKFARSNGLDRR 199 21 6 IPSPTUKARF---IDLSGQKSNPIIPTEFIWNHFNGKIQSTNMKLT----SD TGLMDSAHNHFKRARLFEDLEDEDAEVI PPSSVYPSPLPESTVPANKGYASSAIQTLFTG ADNKIW------FQDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHS PVKAEEPTPTPKIPKKGRKKKNADPEE-----INSSAPRDDDPENRSKFYESASARKR 22 101 112 167 g δ g ò g ઠે 셤

LAEKOWP -- VRCLYKAGRAKFSQGWYEFTLENNLGEGDVCVFELLRT 325 281

200 ECEIDLRDE-----

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221 TVTABERRAINAAKTFEPTNPFFRVVLRPSYLYRGCIMYLPSGFABKYLSGISGFIKVQ 280

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                                                                                                       A; Map position: 2
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004
C;Accession: C84639
R;iin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;iin, X, Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Accession: C84639
A;Accession: C84639
A;Status: preliminary
                                                                                                                              Cyaccession (26593)
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Accession: G86393
A,Status: preliminary
A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Rediques: 1-984 <STO>
A,Cross-references: UNIPROT:Q9LQY4; GB:AE005172; NID:g9295721; PIDN:AAF87027.1; GSPDB:GN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 HNHFKRARLFEDLEDEDAEVIFPSSVYPSPLPESTVPAN--KGYASSAIQTLFTGPVKA- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 HN------INDDDRN----DQINIASRNSSRVKKVRSSLDHSRFVAKVSAW 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 CLSNDRLYIPLSFARLNGLNKINSKKIYLQNEEGRSWKLVLRHDKSGMQTFVQSGWRRFC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 ---EEPTPTP-KIPKKRGRKKKKNADPEEINSSAPRD-----DDPENRSKFYESA---- 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGCIMYLPSGFA----EKYLSGISGFIKVQLAEKQ---WPVRCLYKAGRAKFSQGWYEF 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 RNDLLYLPRSFVNSNRLDKRCS-----EIVLKNEOGGVKWPLVLKRFKSVTYLPKGWTSF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 FFHKLIFSSTIQEKRLRVPDKFVSKF---KDELSVAVALTVPDGHVWRVGLRKADNKIW- 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
            protein T24P13.6 [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C.Accession: G86393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VKMDGLKLTDGWEDFAFAHDLRTGDIVVFRLEGEMVFHVTALGPSCCELQYHT----SS
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7.4%; Score 133.5; DB 2; Length 984;
Best Local Similarity 21.4%; Pred. No. 0.014;
Matches 81; Conservative 46; Mismatches 151; Indels 101;
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332 CQVNRIKAGDSFKFKLVGT 350
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A;Gene: T24P13.6
A;Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 SPYSSYSPSHKQFVTFTLPPDYARIGKLS-LSAPFVRE--NGINKPGEICLLDKHGRKWL 324
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                                                                                                                             10 FFHTLVPSF---HTHLMIPEDFFSEYIEGRSVAELKLDFSDKSWEVKL--SDRRI--TDG
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Novel VRNI polynucleotide sequence encoding a polypeptide which alters vernalization response of plant in which VRNI nucleic acid is expressed, useful for influencing and assessing vernalization phenotype of plants.
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95. .238
/label= region_2
239. .332
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AAG54180
AAG54181
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                                                                                                                                                                                                                protein; 341
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                                                                                                                                                                                                                                               (first entry)
Arabidopsis thaliana
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N-PSDB; AAF62446.
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Levy YY;
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AAB35491;
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                                                                                 US-10-088-187A-11
1796
1 MPRPFFHKLIFSSTIQEKRL........LRTRDFVLKVTAFRVNEYV 341
                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                         2002273
    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                         2002273 segs, 358729299 residues
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Maximum Match 100%
Listing first 45 summaries
                                     sw model
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AAG10757
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ADN73923
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Gapop 10.0 , Gapext 0.5
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Match
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Perfect score:
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The present invention provides the protein and coding sequences of Arabidopsis thaliana VRM1. This protein is capable of altering the vernalisation responses of a plant. Also provided are a number of PCR primers used to isolate the sequences. The sequences are useful in the production of crop plants, where they are able to control the timing of

AAG47303 AAG47302 AAG54199

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flowering, the duration of vernalisation required, the optimum temperature, or even eliminate the need for vernalisation completely. The present sequence is the VRN1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thale cress protein repressed in E2Fa/Dpa expressing plants SeqID 1818.
                                                                                                                                                                                FODGWOEFUDKYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSAFNHFKRA
                                                                                                                                                                                                                          RIFEDLEDEDAEVIPPSSVYPSPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKIP
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                                                                                                                                          MPRPFFHKLIFSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKIW
                                                                                                                    MPRPFFHKLIFSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKIW
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                                                                                             Gaps
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                                                                       Length 341;
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                                                                    Query Match
100.0%; Score 1796; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.4e-167
Matches 341; Conservative 0; Mismatches 0;
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N-PSDB; ADN73922.
                                               Sequence 341 AA;
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This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up conveniently of the conversegulated in transgenic plants oversypresship the heterodimeric EZPa/DPa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or blomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal cransforming storage lipid mobilisation and/or altered photosynthesis, each relative to the corresponding wild type plants. Accordingly, these capacities are also be useful as positive or negative selectable markers during transformation of cells or issues. The identified genes play a cole in a variety of biological processes such as DNA replication, cluming transformation of cells or issues. The identified genes play a cole in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/or carbon metabolism or they function as transcription factors. This polypeptide sequence is thale cress protein expressed by a gene repressed 1.3 fold or more in plants oversexpressing the EZFa/DPa transcription factor, given in an exemplification of the
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.larity 100.0%; Pred. No. 1.4e-167;
Conservative 0; Mismatches 0;
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PR 12-JUL-1999; 99US-0142977P; PR 11-JUL-1999; 99US-01443342P; PR 14-JUL-1999; 99US-01443342P; PR 15-JUL-1999; 99US-0144068P; PR 15-JUL-1999; 99US-0144332P; PR 15-JUL-1999; 99US-0144332P; PR 15-JUL-1999; 99US-0144332P; PR 19-JUL-1999; 99US-0144332P; PR 19-JUL-1999; 99US-0144332P; PR 19-JUL-1999; 99US-0144332P; PR 20-JUL-1999; 99US-0144332P; PR 20-JUL-1999; 99US-0144332P; PR 20-JUL-1999; 99US-0144332P; PR 20-JUL-1999; 99US-0144332P; PR 20-JUL-1999; 99US-0144332P; PR 20-JUL-1999; 99US-014532P; PR 20-JUL-1999; 99US-014532P; PR 20-JUL-1999; 99US-014532P; PR 20-JUL-1999; 99US-014532P; PR 20-JUL-1999; 99US-014532P; PR 20-JUL-1999; 99US-014532P; PR 20-JUL-1999; 99US-014532P; PR 20-JUL-1999; 99US-014532P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-014531P; PR 20-JUL-1999; 99US-0153131P; PR 20-JUL-1999; 99US-0153131P; PR 20-JUL-1999; 99US-0153131P; PR 20-JUL-1999; 99US-0153131P; PR 20-JUL-1999; 99US-0153131P; PR 20-JUL-1999; 99US-0153131P; PR 20-JUL-1999; 99US-0153131P; PR 20-JUL-1999; 99US-0153131P; PR 20-JUL-1999; 99US-0153131P; PR 20-JUL-1999; 99US-0153131P; PR 20-JUL-1999; 99US-0153131P; PR 20-JUL-1999; 99US-0153131P; PR 20-JUL-1999; 99US-0153131P; PR 20-JUL-1999; 99US-0153131P; PR 20-JUL-1999; 99US-0153131P; PR 2

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Arabidopsis thaliana protein fragment SEQ ID NO: 69062
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990S-0139463P.
990S-0139750P.
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Pred. No. 6.6e-167;
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 99US-0160814P.
99US-0160815P.
99US-0160980P.
99US-0160989P.
99US-0161404P.
99US-0161404P.
99US-0161359P.
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99US-0123180P.
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Best Local Similarity 96.1%;
Matches 223; Conservative
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05-MAR.1999;
09-MAR.1999;
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25-MAR.1999;
01-APR.1999;
06-APR.1999;
19-APR.1999;
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llarity 100.0%; Pred. No. 4e-85;
Conservative 0; Mismatches 0; Indels
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99US-0159584P.
99US-0160741P.
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52.7%; Score 946; DB 3;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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81.2%; Pred. No. 2.6e-84;
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Best Local Similarity 81.2%
Matches 190; Conservative
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Protein identification; signal transduction pathway; metabolic pathway;

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hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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14-JUN-1999
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 VKAEEPTPTPKIPKKRGRKKKNADPEEINSSAPRDDDPENRSKFYESASARKRTVTAEER 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 SKAEE---TPKVLKKRGKKKKKNPNPEEVNSSTPGGDDSENRSKFYESASARKRTVTAEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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ERAINAAKTFEPTNPPFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQLAEKQWP 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 VKAEEPTPTPKIPKKRGRKKKNADPEEINSSAPRDDDPENRSKFYESASARKRTVTAEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRCLYKAGRAKFSQGWYEFTLENNLGEGDVCVFELLRTRDFVLKVTAFRVNEYV 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.3%; Score 940; DB 3; Length 226; llarity 80.8%; Pred. No. 1e-83; Conservative 14; Mismatches 19; Indels
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23-SEP-1999;
24-SEP-1999;
              27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Simi
Matches 189;
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Gaps

112

227

55

172

Search completed: December 30, 2004, 06:08:56

Job time : 82 BecB

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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 30, 2004, 06:07:48; Search time 25 Seconds (without alignments) 904.578 Million cell updates/sec Run on:

Title: Perfect score:

US-10-088-187A-11 1796 1 MPRPFFHKLIFSSTIQEKRL......LLRTRDFVLKVTAFRVNEYV 341 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

478139 segs, 66318000 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2_6/ptodata/1/iaa/RecTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:* Issued Patents AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		de					
Result No.	Score	Query Match	Length	DB	ID	Description	
-	97.5	5.4	1178	4	US-09-543-681A-7819	Sequence 7819, Ap	
7	97.5	5.4	8991	4	US-08-714-741-32	Sequence 32, Appl	
m	97	5.4	399	4	US-09-107-532A-6398	Sequence 6398, Ap	
4	95.5	5.3	834	ო	US-08-539-205A-6	Sequence 6, Appli	
S	95.5	5.3	834	4	-09-39	Sequence 6, Appli	
9	94.5	5.3	497	4	US-09-248-796A-15909	Sequence 15909, A	
7	94.5	5.3	693	4	US-09-248-796A-26890	Sequence 26890, A	
80	93.5	5.2	274	4	US-09-489-039A-10361	Sequence 10361, A	
თ	92.5	5.2	194	4	US-08-529-055-64	Sequence 64, Appl	
10	92.5	5.2	496	ო	US-08-740-223A-16	16,	
11	92.5	5.2	496	4	US-09-709-188-16	16,	
12	92	5.1	748	4	US-09-270-767-44371	443	
13	91.5	5.1	1736	4	US-09-919-497-98	98,	
14	90	5.0	1001	4	US-09-762-481B-2	Sequence 2, Appli	
15	88.5	4.0	286	ო	US-08-960-507-20	Sequence 20, Appl	
16	88.5	4.9	286	4	US-09-136-801-20	Sequence 20, Appl	
17	88.5		286	4	US-09-202-088A-20	Sequence 20, Appl	
18	88.5	4.9	334	4	US-09-248-796A-21169	Sequence 21169, A	
19	88.5		480	ო	US-08-740-223A-8	Sequence 8, Appli	
20	88.5	4.9	480	4	US-09-709-188-8	Sequence 8, Appli	
21	88.5	4.9	496		US-08-373-579-6	Sequence 6, Appli	
22	88.5	4.9	496	N	US-08-418-595-6	Sequence 6, Appli	
23	88.5	4.9	496	~	US-08-665-926-6	Sequence 6, Appli	
24	88.5		496	m	US-09-162-437-6	Sequence 6, Appli	
25	88.5	4.9	496	m	US-08-740-223A-6	Sequence 6, Appli	
26	88.5	4.9	496	m	US-09-351-457-4	Sequence 4, Appli	
27	88.5	4.9	496	m	US-09-561-500-4	Sequence 4, Appli	

RESULT 2
US-08-714-741-32
; Sequence 32, Application US/08714741
; Patent No. 6500613
; GENERAL INFORMATION:

645 KNRN 648

444664464444	Sequence 17225, A Sequence 18913, A
099-950-950-950-950-950-950-950-950-950-	US-09-248-796A-17225 US-09-248-796A-18913
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	4 4 5 4

RESULT 1 US-09-543-681A-7819

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Sequence 7819, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION

APPLICANT: GARY BRETON

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

SEQ ID NO S: 8344

SEQ ID NO S: 8344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 KAEEPTPTPKIPKKRKKKNADPEEINSSAPRDDDPENRSKFYESASARKRTVTAEERE 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  477 -VIVPNDQMQTPHFSVIRVRKGEBISSLSYNLA----QYHETQLNBAEDBAVPERKAPEQ
                                                                                                                                                                                                                                                                                                                                                                                                                   15 IQEKRLR------VPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKIWFQDGW
                                                                                                                                                                                                                                                                                                                                                                                                                                             126 -----LEDEDAEVIFPSSVYPSP---LPESTVPANKGYASSAIQTLFTG-----PV
                                                                                                                                                                                                                                                                                                                                          5.4%; Score 97.5; DB 4; Length 1178; 21.7%; Pred. No. 0.47; tive 40; Mismatches 98; Indels 53
                                                                                                                                                                                                                                                                                 ORGANISM: Proteus mirabilis
US-09-543-681A-7819
                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 21.78
Matches 53, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAIN 232
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178 --KIPKKRGRKKKNADPEEINSSAPRDDDPENRS-KFYESASARKRTVTAEERERAINAA 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Calidium; Maureen
APPLICANT: Nefsky, Bradley
TITLE OF INVENTION: Ubsquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: Doston
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
5.4%; Score 97; DB 4; Length 399;
Best Local Similarity 28.9%; Pred. No. 0.095;
Matches 37; Conservative 14; Mismatches 71; Indels
                                                                                                             CURRENT PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEFRONE: (781)893-5007
TELEFRONE: (781)893-507

INFORMATION FOR SEQ ID NO: 6398:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...399
; SEQUENCE DESCRIPTION: SEQ ID NO: 6398:
US-09-107-532A-6398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHERICAL: YES
ORIGINAL SOURCE
ORGANISM: Enterococcus faecium
                                                                              ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-08-539-205A-6
; Sequence 6, Application US/08539205A
; Patent No. 6001619
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COUNTRY: USA
ZIP: 02109-2170
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US-09-107-532A-6398
US-09-107-532A-6398

Sequence 6398, Application US/09107532A

Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

NUMBER OF SEQUENCES: 7310
CORRESPONDENCES: 7310
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
APPLICANT: Briles, David E.
APPLICANT: McDaniel, Larry S.
APPLICANT: Swiatlo, Edwin
APPLICANT: Vother, Janet
APPLICANT: Crain, Marilyn J.
APPLICANT: Tarr, Bebeca
APPLICANT: Brooks Walter, Alexis
APPLICANT: Brooks Walter, Alexis
APPLICANT: Brooks Walter, Alexis
TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
TITLE OF INVENTION: PORTIONS AND PRODUCTS
TITLE OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5721 PAPKPEQP-----BPAPKPEQPAKPEKPAEEPTQPEKFATPKTKVRALKVAE-----F 5768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 RKKKNADPEEINSSAPRDDPENRSKFYESASARKRTVTAEERERAINAAKTFEPTNPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
5.4%; Score 97.5; DB 4; Length 8991;
Best Local Similarity .24.4%; Pred. No. 12;
Matches 38; Conservative 17; Mismatches 72; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER IDUS WE MEDIUM TYPE: Floppy disk MEDIUM TYPE: Ploppy disk COMPUTER: Elam PC Compatible COMPUTER: Ploppy disk COMPUTER: Ploppy disk COMPUTER: Plan PC Compatible COMPUTER: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,741 FILING DATE: 16-SEP-1996 CLASSIFICATION: 4335 ATTORNEY/AGENT INFORMATION: NAME: Prommer Esq., William S. REGISTRATION NUMBER: 25.506 REFERENCE/DOCKET NUMBER: 454312-2460 TELEPONNEICATION INFORMATION: TELEPONE: (212) 840-3333 TELEPONE: (212) 840-3333 TELEPONE: (212) 840-313 TELEPONE: (212) 840-0712 SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: LENGTH: 8991 amino acide TYPE: amino acide STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5769 GVOLRDAGGSNNVGAYFKEGLEETTAEXEAGLGKAE 5804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 RVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQ 280
                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue CITY: New York STATE: New York STATE: Use York ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: amino acid
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6; Gaps

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; TYPE: PRT
; ORGANISM: Candida
US-09-248-796A-15909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 SHSEINYHSTGLMD-------SAHNHFK-RARLFEDLEDEDAEVIFPSSVYP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 SPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPKKRGRKKKNADPEEINSSAPR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 VPEPWETISEEVNIAGDSLGLAL------PPPPVSPGSR-----TSPQELSEELSR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 -----DDDPENRSKFYE-SASARKRTVTAEERERAINAAKTFEPTNPFFRVVLRPSYLY 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 VWRVGLRKADNKIWFQD------GWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09392163A
Patent No. 6503742
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Caligiuri, Maureen
APPLICANT: Nefeky, Bradley
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.3%; Score 95.5; DB 3; Length 834; Best Local Similarity 21.0%; Pred. No. 0.45; Matches 66; Conservative 32; Mismatches 109; Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MPRPFFHKLIFSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDG-
                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

- APPLICATION NUMBER:

FILING DATE: 04-0CT-1995

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REPERENCE/DOCKET NUMBER: 36,709

REPERENCE/DOCKET NUMBER: CSV-005.01

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFEAX: (617) 832-1000

TELEFAX: (617) 832-1000

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 RGCIMYLPSGFAEK 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 VHTTPGLPSGWEER 253
                                                                                                                                                                                                                                                                                                                        LENGTH: 834 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                  US-08-539-205A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-392-163A-6
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RESULT 6

US-09-248-796A-15909

Sequence 15909, Application US/09248796A

Pacent No. 6747137

GENERAL INFORMATION:
APPLICAT: Keith Weinstock et al
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA:
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: 1999-02-12

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 15909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHSEINYHSTGLMD------SAHNHFK-RARLFEDLEDEDAEVIFPSSVYP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 SPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPKKRGRKKKNADPEEINSSAPR 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 RLQITPDSNGEQFSSLIQREPSSRLRSCSVTD---AVAEQGHLPP------PSVAY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 GWEV-VDSNDSASQHQEELPPPPLPPGWEEKVDNLG---------RTYYVNH 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.3%; Score 95.5; DB 4; Length 834; Best Local Similarity 21.0%; Pred. No. 0.45; Matches 66; Conservative 32; Mismatches 109; Indels 107;
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PatentIn Release #1.0, Version #1.30
                                                                                  FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/539,205
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSV-005.01
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 832-1000
TELEPAX: (617) 832-1000
TELEPAX: (617) 832-1000
TELEPAX: (617) 832-1000
TELEPAX: (617) 834 - 000
TELENTH: 834 amino acids
TYPE: amino acid
TYPE: amino acid
                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,163A
FILING DATE:
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240 VHTTPGLPSGWEER 253
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APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBUCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 APSGPRAISR------VQPSYPARAQALRIEGTVRVKFDVSPDGRIDNLQIL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 DIRDED-ARVIPPSSVYPSPLPESTV---PANKGYASSAIQTLFTGPVKAEEPTPTK-- 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEERERAINAAKTFEPTNPFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
5.2%; Score 93.5; DB 4; Length 274;
Best Local Similarity 24.4%; Pred. No. 0.12;
Matches 51; Conservative 20; Mismatches 65; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 64, Application US/08529055
; Sequence 64, Application US/08529055
; Patent No. 6592876
; GENERAL INFORMATION:
   APPLICANT: Briles, David E. APPLICANT: Sviatlo, Edwin
   APPLICANT: Yother, Janet
   APPLICANT: Yother, Janet
   APPLICANT: Yother, Janet
   APPLICANT: Procks Walter, Alexis
   TITLE OF INVENTION: Thereof, Expression Products
   TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
   TITLE OF INVENTION: Portions and Products
   TITLE OF INVENTION: Portions and Products
   MUMBER OF SEQUENCES: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 SAOPANMFEREVKSAMRRW----RYQOGR 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KVQLAEKQWPVRCLYKAGR 296
       Sequence 10361, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,055
FILING DATE: 15-SEP-1995
CLASSIFICATION: 435
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, M
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SOFTWARE: PatentI
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Sequence 26890, Application US/09248796A

Batent No. 6747137

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: AND THERAPEUTICS

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 107196-1132

CURRENT PILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 26890

LENGTH: 693
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                                                                                                                                                                                      66 QEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSAHNHFKRARLFED 125
                                                                                                                                                                                                                                                                                      126 LEDEDAEVIFPSSVYPSPLPESTVPANKGYASSALQTLFTGPVKAEEPTPT------ 176
                                                                                                                                                                                                                                                                                                                     177 --- PKIPKKRGRKKKNADPEEINSSAPRDDDPENRSKFYESASARKRTVTAEERERAINA 233
                                                                                                                                                                                                                                                                                                                                                                                                                407 FGKPSITKKRG-KHRLINKDQVSQGTINDD------FDDGVTYGQBFBFFBRDRA-NY 457
                                                                                                                                                                                                                          312 ------DYFHIFFRNPGDPILFDLONYQHTEVQFIQITSEDKSELHSK----- 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 IFSS-----TIQEKRLRVPD-----KFVSKFKDELSVAVALTVPDGHVWRVG 51
                                                                                           9 LIFSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVG---LRKADNKIWFQDGW 65
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                                                57;
                                                                                                                                   260 LLISNSDQEPIRKQINFGMRDFKNFLNLANFFTTPSSSSERLDENYVTTANN-
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S.3%; Score 94.5; DB 4; Length 693;
Best Local Similarity 20.5%; Pred. No. 0.43;
Matches 54; Conservative 39; Mismatches 116; Indels 5
     Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELPVSSPPVPKRKSSTMKSSSKKSQLNTIIEEDD----STLYDSKE--
                                                  95; Indels
); DB 4;
0.25;
  5.3%; Score 94.5; Di
21.0%; Pred. No. 0.25
tive 40; Mismatches
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US-09-248-796A-26890
                              Best Local Similarity 21.08
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 AKT 236
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458 AET 460
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US-09-248-796A-26890
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            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                 175 PTPKIPKKRGRKKKNADPEEINSSAPRODDPENRSKFYESASARKRTVTAEERERAINAA 234
                                                                                                                                                                                                                                                                                                 Query Match 5.2%; Score 92.5; DB 4; Length 194; Best Local Similarity 28.1%; Pred. No. 0.092; Matches 36; Conservative 17; Mismatches 56; Indels 19
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| Sequence 16, Application US/08740223A
| Sequence 16, Application US/08740223A
| Sequence 16, Application US/08740223A
| Sequence 16, Application US/08740223A
| Sequence 16, Application US/08740223A
| TITLE OF INVENTION: Expressed Ligand - Vascular
| TITLE OF INVENTION: Expressed Ligand - Vascular
| TITLE OF INVENTION: Intercellular Signalling Molecule
| CORRESPONDENCE ADDRESS: 28
| CORRESPONDENCE ADDRESS: |
| STREET: 777 Old Saw Mill Road
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: DISKELLE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASESO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,223A
FILING DATE: 25-OCT-196
CLASSIPTCATION NUMBER: US/08/740,223A
FILING DATE: 02-MUG-199
ATTORNEY/AGENT INFORMATION:
NAWE: CODERT, ROBERT J SA-108
REFERENCE/DOCKET NUMBER: REG 333
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TENGTH: 496 amino acids
             REFERENCE/DOCKET NUMBER: 454312-2400
TELECOMONIACATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INPORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
REGISTRATION NUMBER: 25,506
                                                                                                                                             LENGTH: 194 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                , MOLECULE TYPE: peptide US-08-529-055-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 KTFEPTNP 242
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                                                                                                                                                                                                              linear
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GENERAL INFORMATION:
APPLICANT: Davis et al.
TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
FILE SEFERENCE: REG 333-Z
CURRENT FILING DATE: 100/740,223
PRIOR PILING DATE: 1996-10-25
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 496
                                                                                                                                                                                                                                                                     319 GGGWTIIQRREDGSLDFQKGWKEYKVGFGSPSGEYWLGNEFISQITNQQRYVLKIHLKDW 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319 GGGWTIIQRREDGSLDFQKGWKEYKVGFGSPSGEYWLGNEFISQITWQQRYVLKIHLKDW 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----EFVDRYSIRIGYLL---IFRY 84
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT Homburger et al.
TITLE OF INVEXTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                       ----EFVDRYSIRIGYLL---IFRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.2%; Score 92.5; DB 4; Length 496; Best Local Similarity 29.3%; Pred. No. 0.42; Matches 27; Conservative 16; Mismatches 26; Indels 2:
                                                                                                                                Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.1%; Score 92; DB 4; Length 748; Best Local Similarity 27.2%; Pred. No. 0.91; Matches 44; Conservative 19; Mismatches 63; Indels
                                                                                                                                                                                   26; Indels
                                                                                                                                5.2%; Score 92.5; DB 3; 29.3%; Pred. No. 0.42;
                                                                                                                                                                                                                                                                                                                                                                          379 EGNEAYSLYDHFYISGEELNYRIHLKGLTGTA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 EGNEAYSLYDHFYISGEELNYRIHLKGLTGTA 410
                                                                                                                                                                                                                                                                                                                                            85 EGNSAFSVY-IFNLSHSEINY--HSTGLMDSA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 EGNSAFSVY-IFNLSHSEINY--HSTGLMDSA 113
                                                                                                                                                                                   16; Mismatches
NAME/KEY: hTL2

1 LCARION: 1...496

CTHER INFORMATION: human TIB-2 ligand 2

US-08-740-223A-16
                                                                                                                                                                                                                                       45 GHVWRVGLRKADNKIWFQDGWQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 GHVWRVGLRKADNKIWFQDGWQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 16, Application US/09709188; Patent No. 6441137
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US-09-270-767-44371
                                                                                                                                                                                   27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-09-270-767-44371
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LENGTH: 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-709-188-16
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                                                                                                                                  Query Match
                                                                                                                                                                                   Matches
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SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VYP------GTL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  536 SSSILEKHLTTSRKLLHHH-----SAVNDDDARVLLEFANSKQPPPLAASSTTFVVNA 588
                                                                                           768 DG--WYGALKEAVQQQQNQLVWVSEGKADGATSDDLDLHDDRLSYL----SAPGSEYSMY 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 FTGPVKABEPTPTPKIPKKRGRKKKNADPEEINSSAPRDDDPENRSKFYESASARKRTVT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 AEERERAINAAK-----TEEPINPFF----RVVLRPSYLYRGCIMYL 261
                                                                     152 NKGYASSAIQTLFTGPVKAEEPTPTPKIPKKRGRK----KKNADPEEINSSAPRDDDPEN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09762481B
Patent No. 6632639
GENERAL INFORMATION:
APPLICANT: DOPEZ, MARC
APPLICANT: LOPEZ, PASCAL
TITLE OF INVENTION: MITNAT E. COLI STRAINS, AND THEIR USE FOR PRODUCING
TITLE OF INVENTION: RECOMBINANT POLYPEPTIDES
FILE REFERENCE: USB98APCNREC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 DGHVWRVGLRKA----DNKIWFQDG-----WQEFVDRYSIRIGYLLIFRYEGNSAFSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    822 STDSRHTS-DYEDT---DTEGGAYTDQELDETLNDEVGTPPESAITRSSEPVREDSSGMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Mutter, George L.

TITLE OF INVENTION:
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.0
SEQ ID NO 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95;
SHSEINYHSTGLMDSAHNHFKRARLFEDLEDEDAEVI - - FPSSVYPSPLPEST -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.1%; Score 91.5; DB 4; Length 1736; Best Local Similarity 19.4%; Pred. No. 4; Matches 63; Conservative 41; Mismatches 126; Indels 95;
                                                                                                                                                                                     634 SSSYTSSAAQVQNTLQPPDFNFLYHQATTTATTATYFNPFSR 675
                                                                                                                                                 208 RSKFYESASARKRTVTAEE----RERAINAAKTFEPTNPFFR 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1055 TDQFSRNYEHRLRYEDRVPMYEEQW 1079
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                                                                                                                                                                                                                                                                              Sequence 98, Application US/09919497
Patent No. 6773883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-09-919-497-98
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US-09-919-497-98
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510 MALPSEEFRAERKRPEQPALATFAMPDVPPAPTPAEPAAPVVAPAPKAAPATPAAPAQPG 569
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                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                       5.0%; Score 90; DB 4; Length 1061; 22.9%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                          93 YIFNLSHSEINYHST------GLMDSAHNHFKRARLFEDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 RSKFYESASARK------RTVTAEERERAINAAKT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             626 RSERTEGSDNREENRRNRRQAQQQTABTRESRQQAEVT 663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: 3.5 inch, 1.44 Mb floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                    21; Mismatches
CURRENT APPLICATION NUMBER: US/09/762,481B CURRENT FILING DATE: 2001-08-27 PRIOR APPLICATION NUMBER: PCT/FR99/01879 PRIOR FILING DATE: 1999-07-29 PRIOR FILING DATE: 1998-08-07 PRIOR FILING DATE: 1998-08-07 SUMBER OF SEQ ID NOS: 6 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/08960507
Patent No. 6057435
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF ENGUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P1130p1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
ATTORNEY/AGENT INPORMATION:
NAMB: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-762-481B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650/952-9881
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: WinPati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: Linear
US-08-960-507-20
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 50; Conserv
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                                                                                                                                                                                                     1061
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Query Match
Best Local Similarity 30.4%; Pred. No. 0.47;
Matches 28; Conservative 14; Mismatches 27; Indels 23; Gaps 4;
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Search completed: December 30, 2004, 06:15:51 Job time: 27 secs

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December 30, 2004, 06:10:48; Search time 367 Seconds (without alignments) 334.243 Million cell updates/sec
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| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_PUBFOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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| Cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.pep:*
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| Cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.pep:*
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| Cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1599051 seqs, 359727711 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1796
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

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		Description	Sequence 260947,	Sequence 240434,	Sequence 240433,	Sequence 9287, Ap	Sequence 274348,	Sequence 63507, A	Sequence 157411,	Sequence 166413,	Sequence 192114,	Sequence 178183,	Sequence 203869,	Sequence 152254,	Sequence 129669,
SUMMAKIES		Q QI	US-10-424-599-260947	US-10-424-599-240434	US-10-424-599-240433	US-10-739-930-9287	US-10-425-115-274348	US-10-425-114-63507	US-10-437-963-157411	US-10-424-599-166413	US-10-437-963-192114	US-10-437-963-178183	US-10-437-963-203869	US-10-437-963-152254	US-10-437-963-129669
		- 1	15	15	15	11	11	15	16	15	16	16	16	16	16
		Watch Length DB	431	188	203	344	502	375	402	181	362	750	737	322	306
	% Query	Match	50.6	30.9	20.9	18.3	16.1	15.6	15.5	14.8	14.8	14.0	13.7	13.4	11.9
		Score	908.5	554.5	375.5	329	289.5	280	278	266.5	265	251.5	246	241.5	214
	Result	No.	1	7	e	4	ហ	9	7	æ	σ	10	11	12	13

9 20696 9 31487 9 18715 9 13764	Sequence 162720, Sequence 162720, Sequence 195577, Sequence 232448, Sequence 120554, Sequence 177245,		10566 18875 17045 17045 19557 20720 29203	Sequence 122652, Sequence 122652, Sequence 341488, Sequence 167140, Sequence 221099, Sequence 173953, Sequence 173953,
10-424-599-2 10-425-115-3 10-437-963-1	US-10-424-599-119998 US-10-437-963-162720 US-10-437-963-195577 US-10-424-599-232448 US-10-437-963-120554 US-10-437-963-177245	10-739-930-9695 10-437-963-13842 10-437-963-15691 10-424-599-24199 10-424-599-21659	100-437-963- -10-437-963- -10-437-963- -10-437-963- -10-424-599- -10-437-963-	10-425-115 10-437-963 10-437-963 10-425-115 10-425-115 10-424-599
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210.5 204.5 197 195.5	193 193 186 183 175.5	171.5 170.5 166 165.5 162	145.5 140.5 140.5 140.5 135.5	135.5 134 128.5 127.5 123.5
11 15 17 17 17 17 17 17 17 17 17 17 17 17 17	2210 2210 2310 2310	4 2 2 2 2 2 4 4 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	2 W 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

RESULT 1  US-10-41-599-260947  US-10-41-599-260947  Publication No. US20040031072A1  GENERAL INFORMATION:  APPLICANT: La Rosa Thomas J  APPLICANT: La Rosa Thomas J  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: Can Vordate  APPLICANT: AB APPLICANTON NUMBER: US/10/424,599  CURRENT FILING DATE: 2003-04-28  NUMBER OF SEQ ID NOS: 285684  SEQ ID NO 260947  IENTYH: 431  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PRT  TYPE: PR	Query Match Best Local Similarity 49.7%; Pred. No. 7.1e-76; Matches 198; Conservative 46; Mismatches 95; Indels 59; Gaps 8;	1 MPRPFFHKLIFSSTIQ-EKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKI 59 	60 WFQDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSAHNHFKR 119 	120 A-RLFEDLEDEDAEVIFPSSVYPSPLPESTVPANKGYASSAIQTLFTG- 166
RESULT 1 US-10-424-599-2609 Sequence 260947, Publication No. GENERAL INFORMAT APPLICANT: La R APPLICANT: CAO TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT T	Query Match Best Local S: Matches 198			
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Sequence 9287, Application US/10739930

Publication No. US20040216190A1

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION:
PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION:
PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT PILING DATE: 2003-12-18
SEQ ID NOS: 11088
SEQ ID NOS: 11088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 FKSCNPFFLTVMHRTHISSHGSLANLPMKFCRSHLDLHKCRRLISLQVLSGRIWFAKYQIH 265
                                                                                                                                                                                                                                                                                                             FEPTINPFFRVVLRPSYLYRGCIMYLPSGFAEKYLS--GISGFIKVQ-LAEKQWPVRC-LY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 FFXIITAHNVHEGKLMIPNKFVKKYGKRLQNTLFLKTPNGAEWKMILKKRDGKIWFQKGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 QEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSAHNHFKRARLFED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 LEDEDAEVIFPSSVYPSPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPKKKGR
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                                                                                                                                                                                                                                                                                     182 KRGRKKKNADPEEINSSAPRDDDPENRSKFYESASARKRTVTAEERERAINAAKTFEPTN
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                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                       Length 203;
                                                                                                                                                                                                                                                                                                                                                                    242 PFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQLAE-KQWPV 288
                                                                                                                                                                                                                                                                                                                                                                                         Length 344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: GLYMA-23APR03-C63260_1.p
US-10-739-930-9287
                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_59138C.1.pep
US-10-424-599-240433
                                                                                                                                                                                                     20.9%; Score 375.5; DB 15; 68.5%; Pred. No. 1.4e-26; ive 14; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.3%; Score 329; DB 17; 27.2%; Pred. No. 6.4e-22; tive 57; Mismatches 130;
CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 240433 LENGTH: 203
                                                                                                                                                                                  Query Match
Best Local Similarity 66...
A; Conservative
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ORGANISM: Glycine max
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Matches 94, Conserve
                                                                                  TYPE: PRT
ORGANISM: Glycine
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Sequence 240434, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
EENGTH: 188
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Anoust Sequence Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Cao Yongwei
TITLE OF INVENTION: Sey Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
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CLKFFEEMEGEDSIEISDSSPSHLSPSSLONOALAGSVDKWAMPGKSYNTPPALQNLFNGS 180
                                                                                           241 RKKRKSDGGE--PSAGHEEEVEMRFRFYESASARKRTVTAEERERVINEAKAFEPSNPFC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 YLPSGFAEKYLSGISGFIKVQLAE-KQWPVRCLYKAGRAKFSQGWYEFTLENNLGEGDVC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----PVKAEEPTPTRI------PKKRG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
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                                                                                                                                                                                                                                                 299 RVVLRPSYLYRGCIMYLPSCFAEKHLNGVSGFIKLQISNGRQWPVRCLYKGGRAKLSQGW
                                                                                                                                              RKKKNADPEEINSSAPRODDFENRSKFYESASARKRTVTAEERERAINAAKTFEPTNPFF
                                                                                                                                                                                                                              RVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQLAE-KQWPVRCLYKAGRAKFSQGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 DPENRS----KFYESASARKRTVTAEERERAINAAKTFEPTNPFFRVVLRPSYLYRGCIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Clone ID: PAT_MRT3847_59139C.1.pep
US-10-424-599-240434
                                                                                                                                                                                                                                                                                                                                  359 FEFSLENNLGEGDVCVFELLRMKEVVLQVTIFHVTEDV 396
                                                                                                                                                                                                                                                                                                           304 YEFTLENNLGEGDVCVFELLRTRDFVLKVTAFRVNEYV 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-10-424-599-240433
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US-10-424-599-240434
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125

75

292

RESULT

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TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays
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                                                                                                         APPLICANT: IN CONTINUE.

APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: Application of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the continue of the conti
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APPLICANT: Xovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 PQFFKVFFPEQSTE-RLRIPTMFNQHLKEQQPTGAVSLRGPSGNRWQAALASESESEAAW 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 CFDQGWKEFVTDHSLRLGHFLVFTRDGPAQFSVAVFS-----SSGVIDPAALDARP 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 -FQDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSA---- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 -HNHFKRARLFE-----DLE---DEDAEV-IFPSSVYPSPLPESTVPANKGYASSAI 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 TANGGAAVKLEEGEGVGVRGDVDAGGDTSSEVSLLPAEEGDGGATGRRTGATSGGAGGAS 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 EMSLVLREEGRGVTGKRARATTSDLPADASAPKKHSALAKKAGKRRPQAATSKDVSMIVH 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEATURE:
OTHER INFORMATION: Clone ID: MRT4577_181795C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(502)
OTHER INFORMATION: unsure at all Xaa locations
Sequence 274348, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays
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US-10-425-114-63507
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
III. Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 157411
LENGTH: 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 DLLLFACSGNSSFEVLVFGASGCEKVSSLFGSGLGPDMGKQFNDVVRRHGVHHSVTVSDS 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 E----DTVAPSQLVRSPRNALPLKEPSGKAR------PSKYESPNSSNF1VRHVATGKE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPSYLYR--GCIMYLPSGFAEKYLSGISGFIKVQL--AEKQWPVRCLYKAGRAKFSQ-GW 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 RKNHVQRRNNCLI-IPSKFAADHLGERAHNIILRRPNRKEKWHVSYYHSRHTRCFQNLAL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 RLRVPDKFVSKFKDELSVAVALTVP-DGHVWRVGLRKADNKIWFQDGWQEFVDRYSIRIG
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                                                                                                                                                                                                                                                                                                                                                                                            Length 375;
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
15.6%; Score 280; DB 15; Length 37
Best Local Similarity 27.7%; Pred. No. 2.7e-17;
Matches 89; Conservative 54; Mismatches 136; Indels
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15.5%; Score 278; DB 16; Length 40
Best Local Similarity 26.8%; Pred. No. 4.6e-17;
Matches 103; Conservative 57; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: UC-ZMFLB73255A02_FLI.pep
US-10-425-114-63507
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US-10-437-963-157411
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 63507
LENGTH: 375
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ORGANISM: Oryza sativa
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IYRV 348
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalto David K
APPLICANT: Kovalto David K
APPLICANT: Applicant Applicant Applicant applicant: Solve Yima
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
SEQ ID NOS: 285684
SEQ ID NO 166413
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                                    53 RKADNKIWFQDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDS 112
                                                         148 TVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPK------KRGRKKKNAADPEEIN- 196
                                                                                                                                                                                                                    192 TAVKNEEDADE----LPVCELPASSASPPRHVPEGALDADGGAARRGAAKTRSLQDDLAL 247
                                                                                                                                                                                                                                                             SSAPRDDDPENRSKFYESASARKRTVTAEERERAINAAKTFEPTNPFFRVVLRPSYLYRG 256
                                                                                                                                                                                                                                                                                    302 FWMRFPTGFSRQHLPRERTDVVLRDPGGKVWSV--LYIPNTRDRLSRGWCAFARGNCLEE 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 QDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSA---HNHFK 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
18 RPHFFKVLVGDF--KQRLKIPPNFCKHIPWEESRKAKGLKEASMAATLEGPSGRTWLVVI 75
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                                                                                                                                                                                                                                                                                                                                   257 CIMYLPSGFAEKYL-SGISGFIKVQLAEKQWPVRCLYKAG-RAKFSQGWYEFTLENNLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 RPF-FHKLIFSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKIWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 14.8%; Score 266.5; DB 15; Length 181; Best Local Similarity 34.4%; Pred. No. 1.8e-16; Matches 64; Conservative 33; Mismatches 66; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_121286C.1.pep
US-10-424-599-166413
                                                                                                                                                                                                                                                                                                                                                                                                                               360 GDYCVFELVAAAEF--RVHIFRVVE 382
                                                                                                                                                                                                                                                                                                                                                                                                            GDVCVFELLRTRDFVLKVTAFRVNE 339
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Publication No. US20040031072A1
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ORGANISM: Glycine max
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US-10-437-963-192114
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Sequence 192114, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: APPLICANT: W. Wei

APPLICANT: W. Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Hi, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION NUMBER: US/10/437,963

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 192114
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Sequence 178183, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Each, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
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100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 10
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14.8%; Score 265; DB 16; Length 36
Best Local Similarity 26.6%; Pred. No. 6.4e-16;
Matches 97; Conservative 57; Mismatches 148; Indels
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US-10-437-963-192114
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APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Burbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Fice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: 108/10/437,963
CURRENT PILLNG DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 152254
LENGTH: 322
    97 DFLVFSYDGISKLKVLIFGPSGCEKVHSRSTLKNATHCGEK------- 137
                                                                     WQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSA-HNHFKRARLF 123
                                                                                             207 WAEFANSHDIKMGDFLVFRYTGNSQFEVKIFDPS------GCVKAASHNAVNIGQHA 257
                                                                                                                                                     124 EDLEDEDAEVIFPSSVYPSPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPKKR 183
                                                                                                                                                                                                                                            184 GRKKKNADPEEINSSAPRDDDFENRSKFYESASARKRTVTAEERERAINAAKTFEPTNPF 243
                                                                                                                                                                                                                                                                         292 VIDNCNKKKMFHASSSEDDQ-----ETPTAEVHRMKVEEMVRAIHS-----NHPV 337
                                                                                                                                                                                                                                                                                                                                 244 FRVVLRPSYLYR-GCIMYLPSGFAEKYLSGISGFIKVQLAEKQWPVR-CLYKAGRAKFSQ 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 SAPRDDDPENRSKFYESASARKRT-VTAEERERAINAAKTFEPTNPFFRVVLRPSYLY-R 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: PAT_MRT4530_52323C.1.pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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Best Local Similarity
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APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 203869
                                                                                                                                                                                                                                                                                                             13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 VYPSPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPK--KRG------RKKKN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 ADPEEINSSAPRDDDPENRSKFYESASAR--KRTVTAEERERAINAAKTFEPTNPFFRVV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 LRPSYL--YRGCIMYLPSGFAEXYLSGISGFIKVQLAEK--QWPVRCLYKAG-RAKFSQG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                                                                                 22 VPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKAD-NKIWFQDGWQEFVDRYSIRIGYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 FFHKLIFSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKIWFQDG
                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                           45;
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                                                                                                                                                                                                                                                       ch 14.0%; Score 251.5; DB 16; Length 750; 1 Similarity 26.9%; Pred. No. 3.2e-14; 86; Conservative 55; Mismatches 134; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
13.7%; Score 246; DB 16; Length 737;
Best Local Similarity 23.8%; Pred. No. 1e-13;
Matches 74; Conservative 60; Mismatches 123; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_99011C.1.pep
US-10-437-963-203869
                                                                                                                                                                                                OTHER INFORMATION: Clone ID: PAT_MRT4530_75764C.1.pep
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 178183
LENGTH: 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 203869, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 WYEFTLENNIGEGDVCVFEL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                   ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-437-963-203869
                                                                                                                                                                                                                    US-10-437-963-178183
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APPLICANT: La Rosa: Thomas J.
APPLICANT: La Rovalic, David K.
APPLICANT: Scovalic, David K.
APPLICANT: Scovalic, David K.
APPLICANT: Cahou, Yihua
APPLICANT: Cahou, Yihua
APPLICANT: Cahou, Yongua
TITLE OF INVENTION: Plantes
TITLE OF INVENTION: Plantes
TITLE OF INVENTION: Plantes
TITLE OF INVENTION: Plantes
TITLE OF INVENTION: NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SUGD NO 314879
LENGTH: 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 ARLFEDLEDEDAEVIFPSSVYPSPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----QLNTKKQQETPPI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 PKKRGRKKKNADPEE-----INSSAPRDDDPENRSKFYESASARKRTVT-AEERERAIN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 PAVHFVKIILTTSLADGIL-LPKKFTRKYGDGMSNPVFLKPADGTEWKIHYTKHGGEIWF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 RPFFHKLIFSSTIQEKRLRVPDKFVSKFKDE--LSVAVALTV-PDGHVWRVGLRKADNKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PRPFFHKLIPSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKIWF
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 206969
LENGTH: 164
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                                                                                                                                                                                                                                                                                                                                                                                   DB 15; Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 QKGWKEFATYYSLDHGHLLFFEYEGTSHFDVHIFDSSALEIDYPSHG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 QDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 FFTGGWSQFLDFHGIKNGEVLLLKYEGNMVFKFKAFGLSGCQ---
                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_2891C.1.pep
US-10-424-599-206969
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                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.7%; Score 210.5; DB 15; Best Local Similarity 42.1%; Pred. No. 2.6e-11; Matches 45; Conservative 18; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: MRT4577_50230C.1.pep
US-10-425-115-314879
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OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-425-115-314879
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US-10-437-963-129669
US-10-437-963-129669
Sequence 129669, Application US/10437963
Fublication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wui,
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Bunkharov, Brad
APPLICANT: Bunkharov, Brad
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Bunkharov, Brad
APPLICANT: Bunkharov, Andrey A.
APPLICANT: APPLICANTON: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
SEQ ID NO 129669
SEQ ID NO 129669
EMERGENT FILING DATE: 2003-05-14
EMERGENT: APPLICANTON NUMBER: US/10/437,963
EMERGENT: APPLICANTON NUMBER: US/10/437,963
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; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166, PSEEGLKAELVPGCILPSRIDLTRLQKUILIEKVKAINSETPIYGYVMNNSSIHGIPCTV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRYEGUSAFSVYIFNLSHSEINYHSTGLMDSAHNHFKRARLFEDLEDEDAEVIFPSSVYP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 SPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPKKRGRKKKKNADPEEINSSAPR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 -------SSGCEKVCEKPVDMSGRSYDIAMRNSQDEKKKRKQRDISRQGTVK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 DDDPENRSKFYESASARKRT-VTAEERERAINAAKTFEPTNPFFRVVLRPSYLYR-GCIM 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 YLPSGFAEKYLSGISGFIKVQLAEKQWPVR-CLYKAGRAKFSQGWYEFTLENNLGEGDVC 318
              239 SQTVDICREYADVYLPFKELNWTLQRHGKNWEVLCRTKDTRTKRLSTGWSRFAQENNLQV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 VPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKIWFQDGWQEFVDRYSIRIGYLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.9%; Score 214; DB 16; Length 306; Best Local Similarity 19.7%; Pred. No. 2.9e-11; Matches 63; Conservative 55; Mismatches 137; Indels 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Clone ID: PAT_MRT4530_31904C.1.pep
US-10-437-963-129669
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                                                                                                           299 GDICLFELLKKKEYSMNV 316
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US-10-424-599-206969
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qq	319	319 VKPCNSI-GFRWACTITLKTAINSTR 343
ò	285	285 QMPVR-CLYKAGRAKFSQGWYEFTLENNLGEGDVCVFELLRTR 326
Dp	344	344 SWQVRGTAYKWHRYIIGVGWKSFCQDNRLKAGDLCAFNIIEXR 386
Search completed: De Job time : 368 secs	complet e:368	Search completed: December 30, 2004, 06:22:52 Job time : 368 secs

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